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## (54) Title: HEPATITIS C VIRUS (HCV) POLYPEPTIDES

## (57) Abstract

HCV epitopes useful as immunogenic reagents, and corresponding antibodies and methods of use are disclosed.

P. 4  
P. 27 monoc. poly  
P. 11 - APP general  
Cross-reactive? #20?  
and 49

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HEPATITIS C VIRUS (HCV) POLYPEPTIDES10 Technical Field

The invention relates to materials and methodologies for managing the spread of hepatitis C virus (HCV) infection. More specifically, it relates to polypeptides useful as immunological reagents in the detection, prevention and treatment of HCV infections.

## 15

Background

HCV was first identified and characterized as a cause of non-A, non-B hepatitis (NANBH) by Houghton et al. This led to the disclosure of a number of general and specific polypeptides useful as immunological reagents.

## 20

See, e.g., Houghton et al., EPO Pub. No. 318,216; Houghton et al., EPO Pub. No. 388,232; Choo et al., Science (1989) 244:359-362; Kuo et al., Science (1989) 244:362-364; Houghton et al., Hepatology (1991) 14:381-388. These publications provide the art with an extensive background on HCV generally, as well as the manufacture and uses of HCV polypeptide immunological reagents.

## 25

For brevity, therefore, the disclosure of these publications in particular are incorporated herein by reference.

## 30

Others have readily applied and extended the work of Houghton et al. See, e.g., Highfield et al., UK Pat. App. 2,239,245 (The Wellcome Foundation Ltd.); Wang, EPO Pub. No. 442,394 (United Biomedical Inc.); Leung et al., EPO Pub. No. 445,423 (Abbott Laboratories); Habits et al., EPO Pub. No. 451,891 (Akzo N.V.); Reyes et al., PCT Pub. No. WO 91/15516 (Genelabs Inc.);

Maki et al., EPO Pub. No. 468,657 (Tonen Corp.); and Kamada et al., EPO Pub. No. 469,348 (Shionogi Seiyaku K.K.).

Sensitive, specific methods for screening and identifying carriers of HCV and HCV-contaminated blood or blood products are an important advance in medicine. Post-transfusion hepatitis (PTH) occurs in approximately 10% of transfused patients, and HCV has accounted for up to 90% of these cases. The major problem in this disease is the frequent progression to chronic liver damage (25-55%). Patient care as well as the prevention of transmission of HCV by blood and blood products or by close personal contact require reliable diagnostic and prognostic tools, such as HCV polypeptides, to detect antibodies related to HCV. Such polypeptides are also useful as vaccines and immunotherapeutic therapeutic agents for the prevention and/or treatment of the disease.

Since HCV is a relatively new agent, a continuing need exists to define additional immunological reagents that will allow further study of the clinical course of disease and the epidemiology of HCV in the population.

#### Disclosure of the Invention

The invention pertains to the characterization of new HCV epitopes. The characterization of these epitopes permits the manufacture of polypeptide products which reacted immunologically with antibodies to HCV and/or generate anti-HCV antibody production in vivo. These polypeptide products are useful as standards or reagents in diagnostic tests and/or as components of vaccines. Antibodies, including for example both polyclonal and monoclonal, directed against HCV epitopes contained within these polypeptide sequences are also useful reagents, for example, in diagnostic tests, as therapeutic agents, for screening of antiviral agents, and for the isolation of isolation/purification of HCV polypeptides or particles.

In its broadest sense, the present invention is directed to polypeptides containing the newly characterized HCV epitopes disclosed herein, methods of manufacturing such polypeptides (e.g., recombinant and synthetic methods), methods of using such polypeptides (e.g., diagnostic, vaccine, and therapeutic), and articles of manufacture, compositions or formulations adapted to

such uses (e.g., polypeptides fixed to an immunoassay or other support, oral or injectable pharmaceutical compositions). Similarly, antibodies (polyclonal, monoclonal, or equivalents such as binding fragments, single-chain antigen-binding proteins, etc.) to the HCV epitopes disclosed herein are also included within the

5 scope of the present invention, as well as methods of making such antibodies, methods of using such antibodies (e.g., diagnostic, vaccine, and therapeutic), and articles of manufacture, compositions or formulations adapted to such uses (e.g., antibodies fixed to an immunoassay or other support, oral or injectable pharmaceutical compositions).

10 Other aspects of the invention pertain to kits for analyzing samples for the presence of an HCV antigen comprising the above antibodies in a suitable container. Still other aspects of the invention pertain to kits for analyzing samples for the presence of an antibody directed against an HCV antigen comprising a polypeptide as described above in a suitable container.

15 Still other aspects of the invention are: a method for producing a polypeptide containing the newly disclosed HCV epitopes comprising incubating host cells transformed with an expression vector containing a sequence encoding a polypeptide containing the HCV epitope under conditions which allow expression of said polypeptide; and a polypeptide containing such an HCV epitope produced  
20 by this method.

Immunoassays are also included in the invention. These include an immunoassay for detecting an HCV antigen comprising incubating a sample suspected of containing an HCV antigen with an antibody as described above under conditions which allow the formation of an antigen-antibody complex; and  
25 detecting an antigen-antibody complex containing the antibody. An immunoassay for detecting anti-HCV antibodies comprising incubating a sample suspected of containing anti-HCV antibodies with a polypeptide as described above, under conditions which allow the formation of an antibody-antigen complex; and detecting the antibody-antigen complex containing the polypeptide.

30 Also included in the invention are vaccines for treatment of HCV infection comprising an immunogenic peptide containing an HCV epitope described herein.

Yet another aspect of the invention is a method for producing antibodies to HCV comprising administering to an individual an isolated immunogenic polypeptide containing an HCV epitope described herein in an amount sufficient to produce an immune response.

5 The above aspects of the present invention are accomplished by the discovery of HCV epitopes of the formula

aa<sub>x</sub>-aa<sub>y</sub>,

wherein aa denotes an amino acid;

x and y are integers such that y-x ≥ 6;

10 aa<sub>x</sub>-aa<sub>y</sub> indicates a portion of the amino acid sequence of Figure 1;

and

x is selected from the group consisting of 23-34, 36, 66-79, 81-94,

96-98, 101-103, 186-189, 191, 206, 223, 232, 256, 286, 297-299, 321, 347, 357,

413, 414, 432, 465-471, 480-484, 501, 502, 521, 540-545, 579, 594-599, 601-

15 613, 641, 662-665, 685, 705, 706, 729, 782-789, 801, 851-855, 893, 916, 928,

946, 952-954, 1026, 1072, 1109, 1112-1117, 1218, 1240, 1280-1285, 1322, 1338,

1371, 1384, 1410, 1411, 1454, 1492, 1493, 1532-1535, 1560, 1561, 1566-1568,

1571-1577, 1601-1607, 1615-1620, 1655, 1695, 1710-1712, 1728, 1729, 1758-

1762, 1781, 1808, 1821, 1851, 1880, 1908-1913, 1925, 1940-1948, 1951, 1966-

20 1969, 1999, 2001-2004, 2006-2014, 2024, 2048-2053, 2055-2057, 2071, 2088-

2093, 2108, 2122-2148, 2165, 2187, 2226-2232, 2244-2249, 2267, 2281-2286,

2288, 2289, 2325-2327, 2346, 2347, 2349, 2382, 2401, 2417-2422, 2439-2444,

2446-2456, 2469, 2471-2476, 2495, 2533, 2534, 2573-2578, 2602-2604, 2606-

2612, 2632-2638, 2660, 2676-2679, 2688-2693, 2707, 2721, 2757-2762, 2779,

25 2794, 2795, 2797-2799, 2801, 2802, 2817-2843, 2863-2867, 2878-2884, 2886-

2895.

*Not really*

The above objects are also achieved using HCV epitopes of the formula

aa<sub>x</sub>-aa<sub>y</sub>

wherein aa denotes an amino acid;

5

x and y are integers such that y-x ≥ 6;

aa<sub>x</sub>-aa<sub>y</sub> indicates a portion of the amino acid sequence of Figure 1;

and x is selected from the group consisting of 35 (where y is less than 45), 80 (where y is less than 90), 95 (where y is less than 110), 99 (where y is less than 120), 100 (where y is less than 150), 190 (where y is less than 210), 500

10 (where y is less than 550), 600 (where y is less than 625), 1260 (where y is less than 1280), 1569 (where y is less than 1931), 1570 (where y is less than 1590), 1694 (where y is less than 1735), 1949 (where y is less than 2124), 1950 (where y is less than 1985), 2000 (where y is less than 2050), 2005 (where y is less than 2025), 2054 (where y is less than 2223), 2250 (where y is less than 2330), 2287

15 (where y is less than 2385), 2290 (where y is less than 2310), 2345 (where y is less than 2375), 2348 (where y is less than 2464), 2445 (where y is less than 2475), 2470 (where y is less than 2490), 2605 (where y is less than 2620), 2780 (where y is less than 2830), 2796 (where y is less than 2886), 2800 (where y is less than 2850), and 2885 (where y is less than 2905).

20 In either of the above formula, x-y can be less than or equal to 10, 20, 30, 40 or 50 in some embodiments of the invention.

#### Brief Description of the Drawings

Fig. 1 shows the polyprotein of the HCV prototype isolate HCV1.

25

Fig. 2 shows a composite cDNA sequence for HCV1.

Fig. 3 shows the nucleotide consensus sequence of human isolate 23, variant sequences are shown below the sequence line. The amino acids encoded in the consensus sequence are also shown.

Fig. 4 shows the nucleotide consensus sequence of human isolate

30

27, variant sequences are shown below the sequence line. The amino acids encoded in the consensus sequence are also shown.

Fig. 5 shows the aligned nucleotide sequences of human isolates 23 and 27 and of HCV1. Homologous sequences are indicated by the symbol (\*). Non-homologous sequences are in small letters.

Fig. 6 shows the aligned amino acid sequences of human isolates 23 and 27 and of HCV1. Homologous sequences are indicated by the symbol (\*). Non-homologous sequences are in small letters.

Fig. 7 shows a comparison of the composite aligned nucleotide sequences of isolates Thorne, EC1, HCT #18, and HCV1.

Fig. 8 shows a comparison of the nucleotide sequences of EC10 and 10 a composite of the HCV1 sequence; the EC10 sequence is on the line above the dots, and the HCV1 sequence is on the line below the dots.

Fig. 9 shows a comparison of the amino acid sequences 117-308 (relative to HCV1) encoded in the "EnvL" regions of the consensus sequences of human isolates HCT #18, JH23, JH 27, Thorne, EC1, and of HCV1.

Fig. 10 shows a comparison of the amino acid sequences 330-360 (relative to HCV1) encoded in the "EnvR" regions of the consensus sequences of human isolates HCT #18, JH23, JH 27, Thorne, EC1, and of HCV1.

#### Modes for Carrying Out the Invention

20 Complete citations to publications referred to herein can be found in the "Background" or "Bibliography" sections.

#### L. Definitions

"Hepatitis C virus" or "HCV" refers to the art-recognized viral 25 species of which pathogenic strains cause NANBH, and attenuated strains or defective interfering particles derived therefrom. See generally, publications cited in the section entitled "Background." The HCV genome is comprised of RNA. It is known that RNA containing viruses have relatively high rates of spontaneous mutation, *i.e.*, reportedly on the order of  $10^3$  to  $10^4$  per incorporated nucleotide 30 (Fields & Knipe (1986)). Therefore, since heterogeneity and fluidity of genotype are inherent in RNA viruses, there are multiple strains/isolates, which may be virulent or avirulent, within the HCV species. The propagation, identification,

detection, and isolation of the various HCV strains or isolates has been well documented in the literature. Moreover, the disclosure herein allows the preparation of diagnostics and vaccines for the various strains/isolates, as well as compositions and methods that have utility in screening procedures for anti-viral agents for pharmacologic use, such as agents that inhibit replication of HCV.

Information on several different strains/isolates of HCV is disclosed herein, particularly strain or isolate CDC/HCV1 (also called HCV1). Information from one strain or isolate, such as a partial genomic or amino acid sequence, is sufficient to allow those skilled in the art using standard techniques to isolate new strains/isolates and to identify whether such new strains/isolates are HCV. For example, several different strains/isolates are described below. These strains, which were obtained from a number of human sera (and from different geographical areas), were isolated utilizing the information from the genomic sequence of HCV1.

The information provided herein is indicative that HCV may be distantly related to the flaviviridae. The Flavivirus family contains a large number of viruses which are small, enveloped pathogens of man. The morphology and composition of Flavivirus particles are known, and are discussed in Brinton (1986). Generally, with respect to morphology, Flaviviruses contain a central nucleocapsid surrounded by a lipid bilayer. Virions are spherical and have a diameter of about 40-50 nm. Their cores are about 25-30 nm in diameter. Along the outer surface of the virion envelope are projections that are about 5-10 nm long with terminal knobs about 2 nm in diameter. Typical examples of the family include Yellow Fever virus, West Nile virus, and Dengue Fever virus. They possess positive-stranded RNA genomes (~ 11,000 nucleotides) that are slightly larger than that of HCV and encode a polyprotein precursor of about 3500 amino acids. Individual viral proteins are cleaved from this precursor polypeptide.

The genomic structure and the nucleotide sequence of HCV genomic RNA has been deduced. The genome appears to be single-stranded RNA containing ~ 10,000 nucleotides. The genome is positive-stranded, and possesses a continuous, translational open reading frame (ORF) that encodes a polyprotein of about 3,000 amino acids. In the ORF, the structural protein(s) appear to be

encoded in approximately the first quarter of the N-terminus region, with the majority of the polyprotein responsible for non-structural proteins. When compared with all known viral sequences, small but significant co-linear homologies are observed with the non-structural proteins of the flavivirus family, and with the pestiviruses (which are now also considered to be part of the Flavivirus family).

Based upon the putative amino acids encoded in the nucleotide sequence of HCV1 and other evidence, possible protein domains of the encoded HCV polyprotein, as well as the approximate boundaries, are the following:

10

	<u>Putative Domain</u>	<u>Approximate Boundary</u> (amino acid nos.)
	C (nucleocapsid protein)	<u>1-191</u>
15	E <sub>1</sub> (virion envelope protein)	192-383
	E <sub>2</sub> /NS1 (envelope?)	384-800
20	NS2 (unknown function)	800-1050
	NS3 (protease?)	1050-1650
25	NS4 (unknown function)	1651-2100
	NS5 (polymerase)	2100-3011(end)

These domains are, however, tentative. For example, the E1-NS2 border is probably in the 750-810 region, and NS3-NS4 border is about 1640-1650. There is also evidence that the 191 aa version of C is a precursor that is further processed (e.g., to about 170 aa in length), and that the NS2, NS4 and NS5 proteins are each further processed into two mature proteins.

Different strains, isolates or subtypes of HCV are expected to contain variations at the amino acid and nucleic acids compared with HCV1. Many isolates are expected to show much (*i.e.*, more than about 40%) homology in the total amino acid sequence compared with HCV1. However, it may also be found that there are other less homologous HCV isolates. These would be defined as HCV according to various criteria such as, for example, an ORF of approximately 9,000 nucleotides to approximately 12,000 nucleotides, encoding a polyprotein similar in size to that of HCV1, an encoded polyprotein of similar hydrophobic and/or antigenic character to that of HCV1, and the presence of co-lineair peptide sequences that are conserved with HCV1. In addition, the genome would be a positive-stranded RNA.

HCV encodes at least one epitope which is immunologically identifiable with an epitope in the HCV1 polyprotein. The epitope is unique to HCV when compared to previously known Flaviviruses. The uniqueness of the epitope may be determined by its immunological reactivity with anti-HCV antibodies and lack of immunological reactivity with antibodies to known Flavivirus species. Methods for determining immunological reactivity are known in the art, for example, by radioimmunoassay, by ELISA assay, by hemagglutination, and several examples of suitable techniques for assays are provided herein. Alternatively, a comparison of the sequence of the HCV epitope to previously known sequences of members of the Flavivirus family can be used to evaluate "uniqueness."

In addition to the above, the following parameters of nucleic acid homology and amino acid homology are applicable, either alone or in combination, in identifying a strain/isolate as HCV. Since HCV strains and isolates are evolutionarily related, it is expected that the overall homology of the genomes at the nucleotide level may be about 10% or greater, probably will be

about 40% or greater, probably about 60% or greater, and even more probably about 80% or greater, and in addition that there will be corresponding contiguous sequences of at least about 13 nucleotides. It should be noted that variable and hypervariable regions within the HCV genome; therefore, the homology in these 5 regions is expected to be significantly less than that in the overall genome. The correspondence between the putative HCV strain genomic sequence and, for example, the CDC/HCV1 cDNA sequence can be determined by techniques known in the art. For example, they can be determined by a direct comparison of the sequence information of the polynucleotide from the putative HCV, and the HCV 10 cDNA sequence(s) described herein. For example, also, they can be determined by hybridization of the polynucleotides under conditions which form stable duplexes between homologous regions (for example, those which would be used prior to S<sub>1</sub> digestion), followed by digestion with single stranded specific nuclease(s), followed by size determination of the digested fragments.

15 Because of the evolutionary relationship of the strains or isolates of HCV, putative HCV strains or isolates are identifiable by their homology at the polypeptide level. Generally, HCV strains or isolates are expected to be at least 10% homologous, more than about 40% homologous, probably more than about 70% homologous, and even more probably more than about 80% homologous, and 20 some may even be more than about 90% homologous at the polypeptide level. The techniques for determining amino acid sequence homology are known in the art. For example, the amino acid sequence may be determined directly and compared to the sequences provided herein. Alternatively the nucleotide sequence of the genomic material of the putative HCV may be determined (usually via a 25 cDNA intermediate), the amino acid sequence encoded therein can be determined, and the corresponding regions compared.

As used herein, a polynucleotide "derived from" a designated sequence refers to a polynucleotide sequence which is comprised of a sequence of approximately at least about 6 nucleotides, preferably at least about 8 nucleotides, 30 more preferably at least about 10-12 nucleotides, and even more preferably at least about 15-20 nucleotides corresponding to a region of the designated nucleotide sequence. "Corresponding" means homologous to or complementary to the designated sequence. Preferably, the sequence of the region from which the

polynucleotide is derived is homologous to or complementary to a sequence which is unique to an HCV genome. Whether or not a sequence is unique to the HCV genome can be determined by techniques known to those of skill in the art. For example, the sequence can be compared to sequences in databanks (as of the

- 5 priority date), e.g., Genebank, to determine whether it is present in the uninfected host or other organisms. The sequence can also be compared to the known (as of the priority date) sequences of other viral agents, including those which are known to induce hepatitis, e.g., HAV, HBV, and HDV, and to members of the Flaviviridae. The correspondence or non-correspondence of the derived sequence  
10 to other sequences can also be determined by hybridization under the appropriate stringency conditions. Hybridization techniques for determining the complementarity of nucleic acid sequences are known in the art. See, for example, Maniatis *et al.* (1982). In addition, mismatches of duplex polynucleotides formed by hybridization can be determined by known techniques,  
15 including for example, digestion with a nuclease such as S1 that specifically digests single-stranded areas in duplex polynucleotides. Regions from which typical DNA sequences may be "derived" include but are not limited to, for example, regions encoding specific epitopes, as well as non-transcribed and/or non-translated regions.

- 20 The derived polynucleotide is not necessarily physically derived from the nucleotide sequence shown, but may be generated in any manner, including for example, chemical synthesis or DNA replication or reverse transcription or transcription. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be  
25 consistent with an intended use.

- Similarly, a polypeptide or amino acid sequence "derived from" a designated amino acid or nucleic acid sequence refers to a polypeptide having an amino acid sequence identical to that of a polypeptide encoded in the sequence, or a portion thereof wherein the portion consists of at least 3-5 amino acids, and  
30 more preferably at least 8-10 amino acids, and even more preferably at least 11-15 amino acids, or which is immunologically identifiable with a polypeptide encoded in the sequence. This terminology also includes a polypeptide expressed from a designated nucleic acid sequence.

A recombinant or derived polypeptide is not necessarily translated from a designated nucleic acid sequence; it may be generated in any manner, including for example, chemical synthesis, or expression of a recombinant expression system, or isolation from HCV, including mutated HCV. A recombinant or derived polypeptide may include one or more analogs of amino acids or unnatural amino acids in its sequence. Methods of inserting analogs of amino acids into a sequence are known in the art. It also may include one or more labels, which are known to those of skill in the art.

The term "recombinant polynucleotide" as used herein intends a polynucleotide of genomic, cDNA, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation: (1) is not associated with all or a portion of a polynucleotide with which it is associated in nature, (2) is linked to a polynucleotide other than that to which it is linked in nature, or (3) does not occur in nature.

The term "polynucleotide" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA and RNA. It also includes known types of modifications, for example, labels which are known in the art, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphoro-dithioates, etc.), those containing pendant moieties, such as, for example proteins (including for e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide.

A "purified" polypeptide refers to the polypeptide being in a state that is substantially free of other polypeptides, i.e., in a composition that contains a minimum of about 50% by weight (desired polypeptide/total polypeptide in composition), preferably a minimum of about 70%, and even more preferably a

minimum of about 90% of the desired polypeptide, without regard to non-proteinaceous materials in the composition. Techniques for purifying viral polypeptides are known in the art. Purified antibodies are similarly defined.

"Recombinant host cells", "host cells", "cells", "cell lines", "cell cultures", and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation.

A "replicon" is any genetic element, *e.g.*, a plasmid, a chromosome, a virus, a cosmid, *etc.* that behaves as an autonomous unit of polynucleotide replication within a cell; *i.e.*, capable of replication under its own control.

A "vector" is a replicon in which another polynucleotide segment is attached, so as to bring about the replication and/or expression of the attached segment.

"Control sequence" refers to polynucleotide sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and terminators; in eukaryotes, generally, such control sequences include promoters, terminators and, in some instances, enhancers. The term "control sequences" is intended to include, at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

"Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

An "open reading frame" (ORF) is a region of a polynucleotide sequence which encodes a polypeptide; this region may represent a portion of a coding sequence or a total coding sequence.

- A "coding sequence" is a polynucleotide sequence which is
- 5 transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include, but is not limited to mRNA, cDNA, and recombinant polynucleotide sequences.

10 "Immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptides(s) which are also present in the designated polypeptide(s), usually HCV proteins. Immunological identity may be determined by antibody binding and/or competition in binding; these techniques are known to those of average skill in the art.

15 As used herein, "epitope" refers to an antigenic determinant of a polypeptide. An epitope could comprise 3 or more amino acids that defines the binding site of an antibody. Generally an epitope consists of at least 5 amino acids, and sometimes consists of at least 8 amino acids. Methods of epitope mapping are known in the art.

20 A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly by the kinetics of antibody binding, and/or by competition in binding using as competitor(s) a known polypeptide(s) containing an epitope

25 against which the antibody is directed. The techniques for determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one antibody combining site. An "antibody combining site" or "binding domain" is formed from the folding of variable domains of an antibody molecule(s) to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows an immunological reaction with the antigen. An antibody combining site may be formed from a heavy and/or a

light chain domain ( $V_H$  and  $V_L$ , respectively), which form hypervariable loops which contribute to antigen binding. The term "antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, altered antibodies, univalent antibodies, the Fab proteins, and single domain antibodies.

5 As used herein, a "single domain antibody" (dAb) is an antibody which is comprised of an VH domain, which reacts immunologically with a designated antigen. A dAb does not contain a  $V_L$  domain, but may contain other antigen binding domains known to exist in antibodies, for example, the kappa and lambda domains. Methods for preparing dAbs are known in the art. See, for  
10 example, Ward *et al.* (1989).

Antibodies may also be comprised of  $V_H$  and  $V_L$  domains, as well as other known antigen binding domains. Examples of these types of antibodies and methods for their preparation are known in the art (see, e.g., U.S. Patent No. 4,816,467, which is incorporated herein by reference), and include the following.

15 15 For example, "vertebrate antibodies" refers to antibodies which are tetramers or aggregates thereof, comprising light and heavy chains which are usually aggregated in a "Y" configuration and which may or may not have covalent linkages between the chains. In vertebrate antibodies, the amino acid sequences of all the chains of a particular antibody are homologous with the chains found in one  
20 20 antibody produced by the lymphocyte which produces that antibody *in situ*, or *in vitro* (for example, in hybridomas). Vertebrate antibodies typically include native antibodies, for example, purified polyclonal antibodies and monoclonal antibodies. Examples of the methods for the preparation of these antibodies are described *infra*.

25 25 "Hybrid antibodies" are antibodies wherein one pair of heavy and light chains is homologous to those in a first antibody, while the other pair of heavy and light chains is homologous to those in a different second antibody. Typically, each of these two pairs will bind different epitopes, particularly on different antigens. This results in the property of "divalence", i.e., the ability to  
30 30 bind two antigens simultaneously. Such hybrids may also be formed using chimeric chains, as set forth below.

"Chimeric antibodies", are antibodies in which the heavy and/or light chains are fusion proteins. Typically the constant domain of the chains is

from one particular species and/or class, and the variable domains are from a different species and/or class. Also included is any antibody in which either or both of the heavy or light chains are composed of combinations of sequences mimicking the sequences in antibodies of different sources, whether these sources

- 5      be differing classes, or different species of origin, and whether or not the fusion point is at the variable/constant boundary. Thus, it is possible to produce antibodies in which neither the constant nor the variable region mimic known antibody sequences. It then becomes possible, for example, to construct antibodies whose variable region has a higher specific affinity for a particular antigen, or
- 10     whose constant region can elicit enhanced complement fixation, or to make other improvements in properties possessed by a particular constant region.

Another example is "altered antibodies", which refers to antibodies in which the naturally occurring amino acid sequence in a vertebrate antibody has been varied. Utilizing recombinant DNA techniques, antibodies can be redesigned to obtain desired characteristics. The possible variations are many, and range from the changing of one or more amino acids to the complete redesign of a region, for example, the constant region. Changes in the constant region, in general, to attain desired cellular process characteristics, e.g., changes in complement fixation, interaction with membranes, and other effector functions.

- 15     20    Changes in the variable region may be made to alter antigen binding characteristics. The antibody may also be engineered to aid the specific delivery of a molecule or substance to a specific cell or tissue site. The desired alterations may be made by known techniques in molecular biology, e.g., recombinant techniques, site directed mutagenesis, etc.

- 25     Yet another example are "univalent antibodies", which are aggregates comprised of a heavy chain/light chain dimer bound to the Fc (*i.e.*, constant) region of a second heavy chain. This type of antibody escapes antigenic modulation. See, e.g., Glennie *et al.* (1982).

- 30     Included also within the definition of antibodies are "Fab" fragments of antibodies. The "Fab" region refers to those portions of the heavy and light chains which are roughly equivalent, or analogous, to the sequences which comprise the branch portion of the heavy and light chains, and which have been shown to exhibit immunological binding to a specified antigen, but which lack the

effector Fc portion. "Fab" includes aggregates of one heavy and one light chain (commonly known as Fab'), as well as tetramers containing the 2H and 2L chains (referred to as F(ab)<sub>2</sub>), which are capable of selectively reacting with a designated antigen or antigen family. "Fab" antibodies may be divided into subsets analogous to those described above, i.e., "vertebrate Fab", "hybrid Fab", "chimeric Fab", and "altered Fab". Methods of producing "Fab" fragments of antibodies are known within the art and include, for example, proteolysis, and synthesis by recombinant techniques.

Also included in the term "antibodies" are single-chain antigen-binding (SCA) proteins, such as the type described in the article co-authored by Schlom, J. in the June 15, 1992 issue of Cancer Research (as well as articles cited therein).

As used herein, the term "immunogenic polypeptide" is a polypeptide that elicits a cellular and/or humoral immune response, whether alone or linked to a carrier in the presence or absence of an adjuvant.

The term "polypeptide" refers to a polymer of amino acids and does not refer to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylation, acetylation, phosphorylation and the like. Included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

"Transformation", as used herein, refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, direct uptake, transduction, f-mating or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host genome.

"Treatment" as used herein refers to prophylaxis and/or therapy.

An "individual", as used herein, refers to vertebrates, particularly members of the mammalian species, and includes but is not limited to animals

(e.g., dogs, cats, cattle, swine, sheep, goat, rabbits, mice, rats, guinea pigs, etc.), and primates, including monkeys, chimps, baboons and humans.

As used herein, the "sense strand" of a nucleic acid contains the sequence that has sequence homology to that of mRNA. The "anti-sense strand" contains a sequence which is complementary to that of the "sense strand".

As used herein, a "positive stranded genome" of a virus is one in which the genome, whether RNA or DNA, is single-stranded and which encodes a viral polypeptide(s). Examples of positive stranded RNA viruses include Togaviridae, Coronaviridae, Retroviridae, Picomaviridae, and Caliciviridae.

Included also, are the Flaviviridae, which were formerly classified as Togaviradae. See Fields & Knipe (1986).

As used herein, "antibody containing body component" refers to a component of an individual's body which is a source of the antibodies of interest. Antibody containing body components are known in the art, and include but are not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, white blood cells, and myelomas.

As used herein, a "biological sample" refers to a sample of tissue or fluid isolated from an individual, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs, and also samples of *in vitro* cell culture constituents (including but not limited to conditioned medium resulting from the growth of cells in cell culture medium, putatively virally infected cells, recombinant cells, and cell components).

25

## II. Description of the Invention

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Maniatis, Fitzsch & Sambrook, "Molecular Cloning; A Laboratory Manual" (1982); "DNA Cloning, Volumes I and II" (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed, 1984); "Nucleic Acid Hybridization" (B.D. Hames & S.J. Higgins eds. 1984);

- "Transcription and Translation" (B.D. Hames & S.J. Higgins eds. 1984);  
"Animal Cell Culture" (R.I. Freshney ed. 1986); "Immobilized Cells And  
Enzymes" (IRL Press, 1986); B. Perbal, "A Practical Guide To Molecular  
Cloning" (1984); the series, "Methods in Enzymology" (Academic Press, Inc.);
- 5      "Gene Transfer Vectors For Mammalian Cells" (J.H. Miller and M.P. Calos eds.  
1987, Cold Spring Harbor Laboratory), Meth Enzymol Vol. 154 and Vol. 155  
(Wu and Grossman, and Wu, eds., respectively), Mayer and Walker, eds. (1987),  
"Immunochemical Methods In Cell And Molecular Biology" (Academic Press,  
London); Scopes, (1987) "Protein Purification: Principles and Practice", Second  
10     Edition (Springer-Verlag, N.Y.); and "Handbook of Experimental Immunology",  
Volumes I-IV (D.M. Weir and C. C. Blackwell eds 1986). All patents, patent  
applications, and publications mentioned herein, both *supra* and *infra*, are hereby  
incorporated herein by reference.
- 15     II.A. Truncated HCV Polypeptides  
The useful materials and processes of the present invention are  
made possible by the identification below of new HCV epitopes. The knowledge  
of these epitopes (or antigenic regions) allows for construction of polypeptides  
containing truncated HCV sequences which can be used as immunological  
20     reagents.
- Truncated HCV amino acid sequences encoding at least one viral  
epitope are useful immunological reagents. For example, polypeptides comprising  
such truncated sequences can be used as reagents in an immunoassay. These  
polypeptides also are candidate subunit antigens in compositions for antiserum  
25     production or vaccines. While these truncated sequences can be produced by  
various known treatments of native viral protein, it is generally preferred to make  
synthetic or recombinant polypeptides comprising an HCV sequence. Polypeptides  
comprising these truncated HCV sequences can be made up entirely of HCV  
sequences (one or more epitopes, either contiguous or noncontiguous), or HCV  
30     sequences and heterologous sequences in a fusion protein. Useful heterologous  
sequences include sequences that provide for secretion from a recombinant host,  
enhance the immunological reactivity of the HCV epitope(s), or facilitate the  
coupling of the polypeptide to an immunoassay support or a vaccine carrier. See,

e.g., EPO Pub. No. 116,201; U.S. Pat. No. 4,722,840; EPO Pub. No. 259,149; U.S. Pat. No. 4,629,783, the disclosures of which are incorporated herein by reference.

The size of polypeptides comprising the truncated HCV sequences  
5 can vary widely, the minimum size being a sequence of sufficient size to provide an HCV epitope, while the maximum size is not critical. For convenience, the maximum size usually is not substantially greater than that required to provide the desired HCV epitopes and function(s) of the heterologous sequence, if any. Typically, the truncated HCV amino acid sequence will range from about 5 (or 8)  
10 to about 100 amino acids in length. More typically, however, the HCV sequence will be a maximum of about 50 (or 40) amino acids in length, and sometimes a maximum of about 20, 25 or 30 amino acids. It is usually desirable to select HCV sequences of at least about 8, 10, 12 or 15 amino acids.

Examples of truncated HCV amino acid sequences (octamers) that  
15 are useful as described herein are set forth below in the examples. It is to be understood that these peptides do not necessarily precisely map one epitope. Non-immunogenic portions of the sequence can be defined using conventional techniques and deleted from the described sequences. Further, additional truncated HCV amino acid sequences that comprise an epitope or are immunogenic  
20 can be identified as described herein.

Polypeptide products containing the truncated HCV amino acid sequences disclosed below can be prepared as discrete peptides or incorporated into a larger polypeptide, and may find use as described herein. In preferred applications, truncated sequences from the E1 and/or E2 domains have applications in vaccine and therapeutic products. While generally any of the domains can have some diagnostic utility, C, NS3, NS4 and NS5 are particularly preferred, with combinations of C epitopes with epitopes from one or more of the NS3, NS4 or NS5 domains being particularly preferred.  
25

30 **II.B. Preparation of Polypeptides**

The availability of DNA sequences encoding HCV amino acid sequences permits the construction of expression vectors encoding antigenically active regions of the polypeptide (See, e.g., Fig. 2). These antigenically active

regions may be derived from coat or envelope antigens or from core antigens, or from antigens which are non-structural including, for example, polynucleotide binding proteins, polynucleotide polymerase(s), and other viral proteins required for the replication and/or assembly of the virus particle. Fragments encoding the desired polypeptides are derived, for example, from viral cDNA clones using conventional restriction digestion or by synthetic methods, and are ligated into vectors which may, for example, contain portions of fusion sequences such as  $\beta$ -Galactosidase or superoxide dismutase (SOD), preferably SOD. Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in European Patent Office Publication number 0196056, published October 1, 1986. Vectors encoding fusion polypeptides of SOD and HCV polypeptides, i.e., NANB<sub>3-1-1</sub>, NANB<sub>31</sub>, and C100-3, which is encoded in a composite of HCV cDNAs, are described in Sections IV.B.1, IV.B.2, and IV.B.4, respectively. Any desired portion of the HCV cDNA containing an open reading frame (or a synthetic version thereof), can be used to express a recombinant polypeptide, such as a mature or fusion protein.

Alternatively, a polypeptide contain HCV epitopes can be provided by chemical synthesis using standard techniques based on the amino acid sequence of the figures and the examples.

The DNA encoding the desired polypeptide, whether in fused or unfused form, and whether or not containing a signal sequence to permit secretion, may be ligated into expression vectors suitable for any convenient host. Both eukaryotic and prokaryotic host systems are presently used in forming recombinant polypeptides, and host cell lines is given in EPO Pub. Nos. 318,216. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification may be by techniques known in the art, for example, differential extraction, salt fractionation, chromatography on ion exchange resins, affinity chromatography, centrifugation, and the like. See, for example, Methods in Enzymology for a variety of methods for purifying proteins. Such polypeptides can be used as diagnostics, or those which give rise to neutralizing antibodies may be formulated into vaccines. Antibodies raised against these polypeptides can also be used as diagnostics, or for

passive immunotherapy. In addition, as discussed below, antibodies to these polypeptides are useful for example in isolating and identifying HCV particles.

The HCV polypeptides may also be isolated from HCV virions and truncated (if not already). The virions may be grown in HCV infected cells in tissue culture, or in an infected host.

### II.C. Preparation of Antigenic Polypeptides and Conjugation with Carrier

An antigenic region of a polypeptide is generally relatively small—typically 8 to 10 amino acids or less in length. Fragments of as few as 5

- 10 amino acids may characterize an antigenic region. These segments may correspond to regions of HCV antigen. Accordingly, using the cDNAs of HCV as a basis, DNAs encoding short segments of HCV polypeptides can be expressed recombinantly either as fusion proteins, or as isolated polypeptides. In addition, short amino acid sequences can be conveniently obtained by chemical synthesis.
- 15 In instances wherein the synthesized polypeptide is correctly configured so as to provide the correct epitope, but is too small to be immunogenic, the polypeptide may be linked to a suitable carrier.

A number of techniques for obtaining such linkage are known in the art, including the formation of disulfide linkages using N-succinimidyl-3-(2-

- 20 pyridylthio)propionate (SPDP) and succinimidyl  
4-(N-maleimido-methyl)cyclohexane-1-carboxylate (SMCC) obtained from Pierce Company, Rockford, Illinois, (if the peptide lacks a sulphydryl group, this can be provided by addition of a cysteine residue.) These reagents create a disulfide linkage between themselves and peptide cysteine residues on one protein and an  
25 amide linkage through the epsilon-amino on a lysine, or other free amino group in the other. A variety of such disulfide/amide-forming agents are known. See, for example, *Immun Rev* (1982) 62:185. Other bifunctional coupling agents form a thioether rather than a disulfide linkage. Many of these thio-ether-forming agents are commercially available and include reactive esters of 6-maleimidocaproic acid,  
30 2-bromoacetic acid, 2-iodoacetic acid,  
4-(N-maleimido-methyl)cyclohexane-1-carboxylic acid, and the like. The carboxyl groups can be activated by combining them with succinimide or 1-hydroxyl-2-nitro-4-sulfonic acid, sodium salt. Additional methods of coupling antigens

employs the rotavirus/"binding peptide" system described in EPO Pub. No. 259,149, the disclosure of which is incorporated herein by reference. The foregoing list is not meant to be exhaustive, and modifications of the named compounds can clearly be used.

5 Any carrier may be used which does not itself induce the production of antibodies harmful to the host. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins; polysaccharides, such as latex functionalized Sepharose®, agarose, cellulose, cellulose beads and the like; polymeric amino acids, such as polyglutamic acid, polylysine, and the like; amino acid copolymers; and inactive virus particles, see, for example, Section II.D.  
10 Especially useful protein substrates are serum albumins, keyhole limpet hemocyanin, immunoglobulin molecules, thyroglobulin, ovalbumin, tetanus toxoid, and other proteins well known to those skilled in the art.

In addition to full-length viral proteins, polypeptides comprising  
15

#### II.D. Preparation of Hybrid Particle Immunogens Containing HCV Epitopes

The immunogenicity of the epitopes of HCV may also be enhanced by preparing them in mammalian or yeast systems fused with or assembled with particle-forming proteins such as, for example, that associated with hepatitis B  
20 surface antigen. See, e.g., US 4,722,840. Constructs wherein the HCV epitope is linked directly to the particle-forming protein coding sequences produce hybrids which are immunogenic with respect to the HCV epitope. In addition, all of the vectors prepared include epitopes specific to HBV, having various degrees of immunogenicity, such as, for example, the pre-S peptide. Thus, particles  
25 constructed from particle forming protein which include HCV sequences are immunogenic with respect to HCV and HBV.

Hepatitis surface antigen (HBSAg) has been shown to be formed and assembled into particles in *S. cerevisiae* (P. Valenzuela *et al.* (1982)), as well as in, for example, mammalian cells (P. Valenzuela *et al.* (1984)). The formation of such particles has been shown to enhance the immunogenicity of the monomer subunit. The constructs may also include the immunodominant epitope of HBSAg, comprising the 55 amino acids of the presurface (pre-S) region. Neurath *et al.* (1984). Constructs of the pre-S-HBSAg particle expressible in yeast are disclosed

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in EPO 174,444, published March 19, 1986; hybrids including heterologous viral sequences for yeast expression are disclosed in EPO 175,261, published March 26, 1986. These constructs may also be expressed in mammalian cells such as Chinese hamster ovary (CHO) cells using an SV40-dihydrofolate reductase vector (Michelle *et al.* (1984)).

5 In addition, portions of the particle-forming protein coding sequence may be replaced with codons encoding an HCV epitope. In this replacement, regions which are not required to mediate the aggregation of the units to form immunogenic particles in yeast or mammals can be deleted, thus eliminating 10 additional HBV antigenic sites from competition with the HCV epitope.

#### II.E. Preparation of Vaccines

Vaccines may be prepared from one or more immunogenic polypeptides derived from HCV. These polypeptides may be expressed in 15 various host cells (e.g., bacteria, yeast, insect, or mammalian cells), or alternatively may be isolated from viral preparations or made synthetically. Single- or multi-valent vaccines against HCV may be comprised of one or more epitopes from one or more structural proteins, and/or one or more epitopes from one or more nonstructural proteins. These vaccines may be comprised of, for 20 example, recombinant HCV polypeptides and/or polypeptides isolated from the virions. In particular, vaccines are contemplated comprising one or more of the following HCV proteins, or subunit antigens derived therefrom: E1, E2, C, NS2, NS3, NS4 and NS5. Particularly preferred are vaccines comprising E1 and/or E2, or subunits thereof.

25 In addition to the above, it is also possible to prepare live vaccines of attenuated microorganisms which express one or more recombinant HCV polypeptides. Suitable attenuated microorganisms are known in the art and include, for example, viruses (e.g., vaccinia virus (see Brown *et al.* (1986)), as well as bacteria.

30 The preparation of vaccines which contain an immunogenic polypeptide(s) as active ingredients, is known to one skilled in the art. Typically, such vaccines are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may

also be prepared. The preparation may also be emulsified, or the protein encapsulated in liposomes. The active immunogenic ingredients are often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose,

5 glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants which enhance the effectiveness of the vaccine. Examples of adjuvants which may be effective include but are not limited to: aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trehalose dimycolate and cell 10 wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween® 80 emulsion. The effectiveness of an adjuvant may be determined by measuring the amount of antibodies directed against an immunogenic polypeptide containing an HCV antigenic sequence resulting from administration of this polypeptide in vaccines 15 which are also comprised of the various adjuvants.

20 The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or 25 triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form 30 of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

The proteins may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed

with free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, 5 sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

II.F. Dosage and Administration of Vaccines

10 The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be prophylactically and/or therapeutically effective. The quantity to be administered, which is generally in the range of 5  $\mu$ g to 250  $\mu$ g of antigen per dose, depends on the subject to be treated, capacity of the subject's immune system to synthesize antibodies, and the 15 degree of protection desired. Precise amounts of active ingredient required to be administered may depend on the judgment of the practitioner and may be peculiar to each subject.

The vaccine may be given in a single dose schedule, or preferably in a multiple dose schedule. A multiple dose schedule is one in which a primary 20 course of vaccination may be with 1-10 separate doses, followed by other doses given at subsequent time intervals required to maintain and/or reinforce the immune response, for example, at 1-4 months for a second dose, and if needed, a subsequent dose(s) after several months. The dosage regimen will also, at least in part, be determined by the need of the individual and be dependent upon the 25 judgment of the practitioner.

In addition, the vaccine containing the immunogenic HCV antigen(s) may be administered in conjunction with other immunoregulatory agents, for example, immune globulins.

30 II.G. Preparation of Antibodies Against HCV Epitopes

The immunogenic polypeptides described herein are used to produce antibodies, including polyclonal and monoclonal. If polyclonal antibodies are desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunized

with an immunogenic polypeptide bearing an HCV epitope(s). Serum from the immunized animal is collected and treated according to known procedures. If serum containing polyclonal antibodies to an HCV epitope contains antibodies to other antigens, the polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art, see for example, Mayer and Walker (1987). Alternatively, polyclonal antibodies may be isolated from a mammal which has been previously infected with HCV.

Monoclonal antibodies directed against HCV epitopes can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., M. Schreier *et al.* (1980); Hammerling *et al.* (1981); Kennett *et al.* (1980); see also, U.S. Patent Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against HCV epitopes can be screened for various properties; *i.e.*, for isotype, epitope affinity, etc.

Antibodies, both monoclonal and polyclonal, which are directed against HCV epitopes are particularly useful in diagnosis, and those which are neutralizing are useful in passive immunotherapy. Monoclonal antibodies, in particular, may be used to raise anti-idiotype antibodies.

Anti-idiotype antibodies are immunoglobulins which carry an "internal image" of the antigen of the infectious agent against which protection is desired. See, for example, Nisonoff, A., *et al.* (1981) and Dreesman *et al.* (1985). Techniques for raising anti-idiotype antibodies are known in the art. See, for example, Grzych (1985), MacNamara *et al.* (1984), and Vytdehaag *et al.* (1985). These anti-idiotype antibodies may also be useful for treatment, vaccination and/or diagnosis of NANBH, as well as for an elucidation of the immunogenic regions of HCV antigens.

#### II.H. Immunoassay and Diagnostic Kits

Both the polypeptides and the antibodies of the present invention are useful in immunoassays to detect presence of HCV antibodies, or the presence of

the virus and/or HCV polypeptides (or epitopes), in, for example, biological samples. Design of the immunoassays is subject to a great deal of variation, and many formats are known in the art. The immunoassay will utilize at least one viral epitope derived from HCV. In one embodiment, the immunoassay uses a combination of viral epitopes derived from HCV. These epitopes may be derived from the same or from different viral polypeptides, and may be in separate recombinant or natural polypeptides, or together in the same recombinant polypeptides. An immunoassay may use, for example, a monoclonal antibody directed towards a viral epitope(s), a combination of monoclonal antibodies directed towards epitopes of one viral antigen, monoclonal antibodies directed towards epitopes of different viral antigens, polyclonal antibodies directed towards the same viral antigen, or polyclonal antibodies directed towards different viral antigens. Protocols may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, enzymatic, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays (described below).

Typically, an immunoassay for an anti-HCV antibody(s) will involve selecting and preparing the test sample suspected of containing the antibodies, such as a biological sample, then incubating it with an antigenic (*i.e.*, epitope-containing) HCV polypeptide(s) under conditions that allow antigen-antibody complexes to form, and then detecting the formation of such complexes. Suitable incubation conditions are well known in the art. The immunoassay may be, without limitations, in a heterogenous or in a homogeneous format, and of a standard or competitive type.

In a heterogeneous format, the polypeptide is typically bound to a solid support to facilitate separation of the sample from the polypeptide after incubation. Examples of solid supports that can be used are nitrocellulose (*e.g.*, in membrane or microtiter well form), polyvinyl chloride (*e.g.*, in sheets or microtiter wells), polystyrene latex (*e.g.*, in beads or microtiter plates,

polyvinylidene fluoride (known as Immulon®), diazotized paper, nylon membranes, activated beads, and Protein A beads. For example, Dynatech Immulon® 1 or Immulon® 2 microtiter plates or 0.25 inch polystyrene beads (Precision Plastic Ball) can be used in the heterogeneous format. The solid support containing the 5 antigenic polypeptide is typically washed after separating it from the test sample, and prior to detection of bound antibodies. Both standard and competitive formats are known in the art.

In a homogeneous format, the test sample is incubated with antigen 10 in solution. For example, it may be under conditions that will precipitate any antigen-antibody complexes which are formed. Both standard and competitive formats for these assays are known in the art.

In a standard format, the amount of HCV antibodies forming the antibody-antigen complex is directly monitored. This may be accomplished by determining whether labeled anti-xenogenic (e.g., anti-human) antibodies which 15 recognize an epitope on anti-HCV antibodies will bind due to complex formation. In a competitive format, the amount of HCV antibodies in the sample is deduced by monitoring the competitive effect on the binding of a known amount of labeled antibody (or other competing ligand) in the complex.

Complexes formed comprising anti-HCV antibody (or, in the case of 20 competitive assays, the amount of competing antibody) are detected by any of a number of known techniques, depending on the format. For example, unlabeled HCV antibodies in the complex may be detected using a conjugate of antixenogeneic Ig complexed with a label, (e.g., an enzyme label).

In immunoassays where HCV polypeptides are the analyte, the test 25 sample, typically a biological sample, is incubated with anti-HCV antibodies under conditions that allow the formation of antigen-antibody complexes. Various formats can be employed. For example, a "sandwich assay" may be employed, where antibody bound to a solid support is incubated with the test sample; washed; incubated with a second, labeled antibody to the analyte, and the support is washed again. Analyte is detected by determining if the second antibody is bound to the 30 support. In a competitive format, which can be either heterogeneous or homogeneous, a test sample is usually incubated with antibody and a labeled,

competing antigen is also incubated, either sequentially or simultaneously. These and other formats are well known in the art.

Efficient detection systems for HCV infection may include the use of panels of epitopes, as described above. The epitopes in the panel may be constructed into one or multiple polypeptides. The assays for the varying epitopes may be sequential or simultaneous.

The enzyme-linked immunosorbent assay (ELISA) can be used to measure either antigen or antibody concentrations. This method depends upon conjugation of an enzyme to either an antigen or an antibody, and uses the bound enzyme activity as a quantitative label. To measure antibody, the known antigen is fixed to a solid phase (e.g., a microplate or plastic cup), incubated with test serum dilutions, washed, incubated with anti-immunoglobulin labeled with an enzyme, and washed again. Enzymes suitable for labeling are known in the art, and include, for example, horseradish peroxidase. Enzyme activity bound to the solid phase is measured by adding the specific substrate, and determining product formation or substrate utilization colorimetrically. The enzyme activity bound is a direct function of the amount of antibody bound.

To measure antigen, a known specific antibody is fixed to the solid phase, the test material containing antigen is added, after an incubation the solid phase is washed, and a second enzyme-labeled antibody is added. After washing, substrate is added, and enzyme activity is estimated colorimetrically, and related to antigen concentration. Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the polypeptides of the invention containing HCV epitopes or antibodies directed against HCV epitopes in suitable containers, along with the remaining reagents and materials required for the conduct of the assay, as well as a suitable set of assay instructions.

### III. General Methods

The general techniques used in the practice of the present invention can be found in, for example, the references cited herein, particularly EPO Pub. Nos. 318,216 and 388,232, as well as the references in the bibliography, which are incorporated herein by reference.

#### **IV. Examples**

Described below are examples of the present invention which are provided only for illustrative purposes, and not to limit the scope of the present invention. In light of the present disclosure, numerous embodiments within the scope of the claims will be apparent to those of ordinary skill in the art.

##### **IV.A. Epitope Mapping of HCV Genome**

The following example is the result of an epitope mapping experiment conducted on the HCV1 polyprotein sequence shown in Fig. 1. As shown in Fig. 3-11, there are heterogeneities among HCV isolates, indicating that these amino acid substitutions can be made in the octamers described below. In addition to substitutions with amino acids from the corresponding location in other HCV isolates, substitutions with synthetic analogs of the particular amino acids or conservative substitutions based on charge, etc. (particularly when the substitution does not destroy antibody binding) are within the scope of the invention.

##### **IV.A.1. Synthesis of Overlapping Peptides**

Polyethylene pins arranged on a block in an 8×12 array (Coselco Mimetopes, Victoria, Australia) were prepared by placing the pins in a bath (20% v/v piperidine in dimethylformamide (DMF)) for 30 minutes at room temperature. The pins were then removed, washed in DMF for 5 min, then washed in methanol four times (2 min/wash). The pins were allowed to air dry for at least 10 min, then washed a final time in DMF (5 min). 1-Hydroxybenzotriazole (HOBr, 367 mg) was dissolved in DMF (80 mL) for use in coupling Fmoc-protected amino acids: Fmoc-L-Ala-OPfp, Fmoc-L-Cys(Tyr)-OPfp, Fmoc-L-Asp(O-tBu)-OPfp, Fmoc-L-Glu(O-tBu)-OPfp, Fmoc-L-Phe-OPfp, Fmoc-Gly-OPfp, Fmoc-L-His(Boc)-OPfp, Fmoc-L-Ile-OPfp, Fmoc-L-Lys(Boc)-OPfp, Fmoc-L-Leu-OPfp, Fmoc-L-Met-OPfp, Fmoc-L-Asn-OPfp, Fmoc-L-Pro-OPfp, Fmoc-L-Gln-OPfp, Fmoc-L-Arg(Mtr)-OPfp, Fmoc-L-Ser(t-Bu)-ODhbt, Fmoc-L-Thr(t-Bu)-ODhbt, Fmoc-L-Val-OPfp, and Fmoc-L-Tyr-OPfp.

The protected amino acids were placed in microtiter plate wells with HOBr, and the pin block placed over the plate, immersing the pins in the wells. The assembly was then sealed in a plastic bag and allowed to react at 25°C for 18

hours to couple the first amino acids to the pins. The block was then removed, and the pins washed with DMF (2 min), MeOH (4 × 2 min), and again with DMF (2 min) to clean and deprotect the bound amino acids. The procedure was repeated for each additional amino acid coupled, until all octamers had been prepared.

5                  The free N-termini were then acetylated to compensate for the free amide, as most of the epitopes are not found at the N-terminus and thus would not have the associated positive charge. Acetylation was accomplished by filling the wells of a microtiter plate with DMF/acetic anhydride/triethylamine (5:2:1 v/v/v) and allowing the pins to react in the wells for 90 min at 20°C. The pins were 10                  then washed with DMF (2 min) and MeOH (4 × 2 min), and air dried for at least 10 min.

15                  The side chain protecting groups were removed by treating the pins with trifluoroacetic acid/phenol/dithioethane (95:2.5:2.5, v/v/v) in polypropylene bags for 4 hours at room temperature. The pins were then washed in dichloromethane (2 × 2 min), 5% di-isopropylethylamine/dichloromethane (2 × 5 min), dichloromethane (5 min), and air-dried for at least 10 min. The pins were then washed in water (2 min), MeOH (18 hours), dried *in vacuo*, and stored in sealed plastic bags over silica gel.

20

#### IV.A.2. Assay of Peptides

Octamer-bearing pins prepared as above were first treated by sonicating for 30 min in a disruption buffer (1% sodium dodecylsulfate, 0.1% 2-mercaptoethanol, 0.1 M NaH<sub>2</sub>PO<sub>4</sub>) at 60°C. The pins were then immersed several 25 times in water (60°C), followed by boiling MeOH (2 min), and allowed to air dry. The pins were then precoated for 1 hour at 25°C in microtiter wells containing 200 μL blocking buffer (1% ovalbumin, 1% BSA, 0.1% Tween®, and 0.05% NaN<sub>3</sub> in PBS), with agitation. The pins were then immersed in microtiter wells containing 175 μL antisera obtained from human patients diagnosed as having 30 HCV and allowed to incubate at 4°C overnight. The pins were assayed against antisera from three individual patients. Specimen #PAA 3663-s ("A") exhibited strong reaction to HCV Western blots, HCV competitive ELISA, HCV ELISA to clone C100-3 (at 1:1000 dilution), and RIBA responses of >4+ to C100, 5-1-1,

and C33c (C22 not done). (Antigen/clone names are per EPO Pub. Nos. 318,216 and 388,232, as well as those described in the literature regarding HCV immunoassays available from Ortho Diagnostics Systems, Inc.) Neat plasma was diluted 1:500 in blocking buffer. Specimen #PAA 33028 ("B") exhibited strong reaction to HCV Western blots, HCV competitive ELISA, HCV ELISA to clone C100-3 (at 1:500 dilution), and RIBA responses of >4+ to C100, 5-1-1, C33C and C22. Polyclonal antisera was partially purified by passage through a protein A column, and was used at a dilution of 1:200 in blocking buffer. Specimen #PAA s32931 ("C") exhibited moderate reaction to HCV Western blots (3+), HCV competitive ELISA, HCV ELISA to clone C100-3 (at 1:64 dilution), and RIBA responses of 3+ and 4+ to C100 and 5-1-1, respectively (C33c and C22 not done). Polyclonal antisera was partially purified by passage through a protein A column, and was used at a dilution of 1:500 in blocking buffer.

The pins were washed in PBS/Tween® 20 (4 × 10 min) at room temperature, then incubated in microtiter wells containing horseradish peroxidase-labeled goat anti-Human Ig antisera (175 µL, 1:2000 dilution in blocking buffer without NaN<sub>3</sub>) for 1 hour at 25°C with agitation. The antihuman antisera is specific for human Ig light and heavy chains, and reacts with both IgG and IgM classes. The pins were again washed in PBS/Tween® 20 (4 × 10 min) at room temperature. Substrate solution was prepared by diluting NaH<sub>2</sub>PO<sub>4</sub> (1 M, 200 mL) and citric acid (1 M, 160 mL) to 2 L with distilled water, adjusting the pH to 4.0. Azino-di-3-ethylbenzthiazodinsulfonate (ABTS, 50 mg) and hydrogen peroxide (0.3 µL/mL) was added to 100 mL of buffer immediately prior to use to complete the substrate solution. The substrate solution (150 µL) was added to each well of a microtiter plate, and the pins immersed in the wells and incubated at 25°C in the dark. After color developed, the reactions were halted by removing the pins, and absorbance of the solutions read at 405 nm.

The octamers listed below were immunoreactive with anti-HCV antisera. Peptides reacting with all three antisera are listed as epitopes, while peptides reacting with only one or two antisera are listed as weak epitopes (indicated by " - "). Particularly strong epitopes are labeled with letters rather than numbers (e.g., EpAA).

	<u>AA# Sequence</u>	<u>AA# Sequence</u>
5	23 KEPGGGQQA 24 EPGGGQAV 25 PGGGQAVVG 26 GGGQAVGGV 27 GGQAVGGV 28 GQAVGGVY 29 QAVGGVYL ~	Ep2 87 GNEGCGWA 88 NEGCGWAG 89 EGCGWAGW 90 GCGWAGWL 91 CGWAGWL 92 GWAGWL 93 WAGWLSP 94 AGWLSPR 95 GWLLSPRG 96 WLLSPRGS 97 LLSPRGSR 98 LSPrGSRP 99 SPRGSRPS
10	30 AVGGVYLL 31 VGGVYLLP 32 GGVYLLPR 33 GVYLLPRR 34 VYLLPRRG 35 YLLPRRG 36 LLPRRGPR	
15		
20	66 PKARRPEG Ep1 67 KARRPEGR 68 ARRPEGRT 69 RRPEGRTW 70 RPEGRTWA 71 PEGRTWAQ 72 EGRTWAQP 73 GRTWAQPG EpA	100 PRGSRPSW Ep3 101 RGSRPSWG 102 GSRPSWGP 103 SRPSWGPT
25	74 RTWAQPGY 75 TWAQPGYP 76 WAQPGYPW 77 AQPGYPWP 78 QPGYPWP 79 PGYPWP 80 GYPWP 81 YPWPL 82 PWPL 83 WPL 84 PLY 85 LYG 86 YGN	186 TVPASAYQ Ep4 187 VPASAYQV 188 PASAYQVR 189 ASAYQVRN 190 SAYQVRNS 191 AYQVRNST
30	87 GCG 88 GCG 89 GCG 90 GCG 91 GCG 92 GCG 93 GCG 94 GCG 95 GCG 96 GCG 97 GCG 98 GCG 99 GCG	206 DCPNSSIV ~
35	100 PRGSRPSW 101 RGSRPSWG 102 GSRPSWGP 103 SRPSWGPT	223 TPGCVPCV ~
40	186 TVPASAYQ 187 VPASAYQV 188 PASAYQVR 189 ASAYQVRN 190 SAYQVRNS 191 AYQVRNST	232 EGNASRCW Ep5
45	206 DCPNSSIV ~	256 TQLRRHID ~
	286 LVGQLFTF ~	321 MMMNWSP ~
	297 RHWTTQGC Ep6	347 DMIAGAHW Ep7
	298 HWTTQGCN	357 LAGIAYFS Ep8
	299 WTTQGCNC	

	413	LINTNGSW EpB	594	YSRCGSGP F <sub>A</sub>
	414	INTNGSWH	595	SRCGSGPW
5	432	SLNTGWLA -	596	RCGSGPWL
	465	FDQGWGPI EpC	597	CGSGPWLT
	466	DQGWGPI	598	GSGPWLT
	467	QGWGPISY	599	SGPWLT
	468	GWGPISYA	600	GPWLTPRC
10	469	WGPISYAN	601	PWLTPRCL
	470	GPISYANG	602	WLTPRCLV
	471	PISYANGS	603	LTPRCLVD EpF
	480	PDQRPYCW EpD	604	TPRCLVDY
15	481	DQRPYCWH	605	PRCLVDYP
	482	QRPYCWHY	606	RCLVDYPY
	483	RPYCWHYP	607	CLVDYPYR
	484	PYCWHYPP	608	LVDYPYRL
20	500	KSVCGPVY Ep9	609	VDYPYRLW
	501	SVCGPVYC	610	DYPYRLWH
	502	VCGPVYCE	611	YPYRLWHY F <sub>B</sub>
	521	RSGAPTYS Ep10	612	PYRLWHYP
25	540	NNTRPPLG EpE	613	YRLWHYPC
	541	NTRPPLGN	641	EAACNWTR
	542	TRPPLGNW		
	543	RPPLGNWF		
30	544	PPLGNWFG	662	LSPLLLII Ep13
	545	PLGNWFGC	663	SPLLIII
	546	LGNWFGCT	664	PLLIIHQ
	547	GNWFGCTW	665	LLLIIQW
	548	NWFGCTWM		
35	549	WFGCTWMN	685	LSTGLIHL -
	579	LHCPTDCF -	705	VGSSIASW -
			706	GSSIASWA
			729	ARVCSCIW Ep14
			782	WVPGAVYT
40			783	VPGAVYTF
			784	PGAVYTFY
			785	GAVYTFYG
			786	AVYTFYGM
45			787	VYTFYGMW
			788	YTFYGMWP
			789	TFYGMWPL
			801	LALPQRAY -

	851	RVEAQLHV EpH	1384	VIKGGGRHL Ep20
	852	VEAQLHVVW	1410	LGINAVAY Ep21
	853	EAQLHVVWI	1411	GINAVAYY
	854	AQLHVVWIP		
5	855	QLHVVWIPP	1454	CNTCVIQT ~
	893	LAVFGPLW ~	1492	GRGKPGIY Ep22
	916	QGLLRFCA ~	1493	RGKPGIYR
10	928	MIGGHYVQ Ep15	1532	PAETTVRL Ep23
	946	TGTYYVYNH EpI	1533	AETTVRLR
			1534	ETTVRLRA
			1535	TTVRLRAY
15	952	NHLIPLRD EpJ		
	953	HLTPLRDW	1560	GVFIGLIH Ep24
	954	LTPLRDWA	1561	VFIGLIHI
	1026	LAPITAYA ~	1581	ENLPYLVA
20	1072	TCINGVCW EpK	Ep25	1567 NLPYLVAY
	1109	LVGWPAPQ Ep16		1568 LPYLVAYQ
	1171	CPAGHAVG Ep17		1569 PYLVAYQA
	1113	PAGHAVGI		1570 YLVAYQAT
	1114	AGHAVGIF		1571 LVAYQATV
	1115	GHAVGIFR		1572 VAYQATVC
	1116	HAVGIFRA		1573 AYQATVCA
30	1117	AVGIFRAA		1574 YQATVCAR
	1218	VVPQSEQV EpL		1575 QATVCARQ
	1240	VPAAYAAQ ~	Ep26	1576 ATVCARQA
35	1260	ATLGFGAY ~		1577 TVCARQAP
	1280	GVRITTGS Ep18		1601 PPSWDQMW
	1281	VRITTGSP		1602 PSWDQMWK
	1282	RITTGSPI		1603 SWDQMWKC
	1283	ITTGSPIT		1604 WDQMWKCL
	1284	TTGSPITY		1605 DQMWKCLI
	1285	TGSPITYG		1606 QMWKCLIR
40				1607 MWKCLIRL
	1283	ITTGSPIT		1615 KPTLHGPI Ep27
	1284	TTGSPITY		1616 PTLHGPIP
	1285	TGSPITYG		1617 TLHGPIPL
45	1322	DATSILGI ~		1618 LHGPILL
	1338	TAGARLVV ~		1619 HGPIPLL
	1371	GEIPFYGK Ep19		1620 GPILLLRY
			1655 VVTSTWVL ~	

	1694	IIPDREVL EpM	1966	SECTIPCS Eps
	1695	IPDREVLY	1967	ECTIPCSG
5	1710	ECSQHLPY EpN	1968	CTIPCSGS
	1711	CSQHLPYI	1969	TIPCSGSW
	1712	SQHLPYIE	1999	LMPQLPGI Ept
	1728	EKQKALGL EpO	2000	MPQLPGIP
10	1729	KQKALGLL	2001	PQLPGIPE
	1758	EIEWAKLM EpP	2002	QLPGIPEV
	1759	IEWAKLMW	2003	LPGIPEVS
	1760	EWAKLWN	2004	PGIPEVSC
	1761	WAKLMWNE	2005	GIPEVSCQ
15	1762	AKLMWNEI	2006	IPEVSCQR
	1781	LPGNPAIA -	2007	PEVSCQRG
	1808	LFNILGGW Ep28	2008	EVSCQRGY
20	1821	AAPGAATA -	2009	VSCQRGYK
	1851	ILAGYGAG Ep29	2010	SCQRGYKG
	1880	VNLPAIL -	2011	CQRGYKGV
25	1908	PGEHAVQW EpG	2012	QRGYKGVW
	1909	GEGAVQWM	2013	RGYKGVWR
	1910	EGAVQWMN	2014	GYKGVWRG
30	1911	GAVQWMNR	Ep31	
	1912	AVQWMNRL		
	1913	VQWMNRLI		
	1925	RGNHVSPI EpR	2024	IMHTRCHC
35	1940	AAARVTAI Ep30	2048	VGPRICRN Epu
	1941	AARVTAIL	2049	GPRICRNY
	1942	ARVTAILS	2050	PRICRNYW
	1943	RVTAILSS	2051	RICRNYWS
40	1944	VTAILSSL	2052	ICRNYWSG
	1945	TAILSSLV	2053	CRNYWSGT
	1946	AISSLVLT	2054	RNYWSGTE
	1947	ILSSLVTQ	2055	NYWSGTEP
	1948	LSSLVTQL	2056	YWSGTEPI
45	1949	SSLVTQLL	2057	WSGTEPIN
	1950	SLVTQLLR	2071	TPLPAPNY Ep32
	1951	LVTQLLRR	2088	EYVIRQV EpV
			2089	EYVIRQVG
			2090	YVIRQVGD
			2091	VIRQVGDF
			2092	IRQVGDFH
			2093	RQVGDFHY
			2108	DNLKCPCQ -

	2122	EELDGVR EpW	2280	REAQALPV EpZ
	2123	IELDGVRL	2281	EAQALPVW
	2124	ELDGVR LH	2282	AQALPVWA
	2125	LDGVR LER	2283	QALPVWAR
5	2126	DGVRL HRF	2284	ALPVWARP
	2127	GVR LHRFA	2285	LPVWARP D
	2128	VRL HRFAP	2286	PVWARP DY
	2129	RLH RFAPP	2287	VWARP DYN
	2130	LHR FAPP C	2288	WARP DYN P
10	2131	HRF APP CK	2289	ARP DYN PP
	2132	RF APP CKP	2290	RPDYN PPL
	2133	FAPP CKPL		
	2134	APP CK PLL	2325	PPPRKKRT Ep35
	2135	PPCK PLL R	2326	PPRK RT V
15	2136	PCK PLL RE	2327	PRKK RT VV
	2137	CK PLL REE		
	2138	KPLL REEV	2345	AELASRSE Ep36
	2139	PLL REEV S	2346	ELASRSEG
	2140	LL REEV SF EpX	2347	LASRSEGS
20	2141	L REEV SF R	2348	ASRSEGSS
	2142	REEV SF RV	2349	SRSEGSSS
	2143	EEV SF RV G		
	2144	EVS FR V GL	2382	AESYSSMP Ep37
	2145	VS FR V GL H		
25	2146	SFR V GL HE	2401	SDGS WST V
	2147	FR V GL HE Y		
	2148	RV GL HE Y P		
			Ep38	
	2165	EPEPDV AV ~	2417	VVCCSMSY
30	2187	GR RL A R GS ~	EpAA	
			2418	VCCSMSY W
	2226	LIEAN LLW EpY	2419	CCSMSY WI
	2227	IEAN LLWR	2420	CSMSY WIG
35	2228	EAN LLWR Q	2421	SMSY WIGA
	2229	AN LLWR QE	2422	MSY WIGAL
	2230	NLL WR QEM		
	2231	LLWR QEM MG		
	2232	LWR QEM GG		
40	2244	VESEN KVV Ep33		
	2245	ESEN KVV VI		
	2246	SEN KVV IL		
	2247	ENK VVILD		
45	2248	NKV VILD S		
	2249	KVVILD SF		
	2250	VVILD SFD		
	2267	EISVPAHI Ep34		

	2439	QKLPINAL EpBB		2602	LPLAVMGS
5	2440	KLPINALS	EpDD	2603	PLAVMGSS
	2441	LPINALSN		2604	LAVMGSSY
	2442	PINALSNS		2605	AVMGSSYG
	2443	INALSNSL		2606	VMGSSYGE
	2444	NALSNSLL		2607	MGSSYGEQ
	2445	ALSNSSLR		2608	GSSYGEQR
10	2446	LSNSLLRH		2609	SSYGEQRV
	2447	SNSLLRHH		2610	SYGEQRVE
	2448	NSLLRHNN		2611	YGEQRVEE
	2449	SLLRHHL		2612	GEQRVEEL
	2450	LLRHHLNV			
	2451	LRHHNLVY			
	2452	RHHNLVYS		2632	KTPMGFSY
15	2453	HHLVYST	Ep41	2633	TPMGFSYD
	2454	HNLVYSTI		2634	PMGFSYDT
	2455	NLVYSTIS		2635	MGFSYDTR
	2456	LVYSTISR		2636	GFSYDTRC
20	2469	QKKVTFDR Ep39		2637	FSYDTRCE
	2470	KKVTFDRL		2638	SYDTRCED
	2471	KVTFDRLQ			
	2472	VTFDRLQV		2660	YQCCDLDP ~
	2473	TFDRLQVL			
25	2474	FDRQLVLD		2676	LTERLYVG
	2475	DRLQVLDS	EpEE	2677	TERLYVGG
	2476	RLQVLDSH		2678	ERLYVGGP
	2495	ASKVKANL ~		2679	RLYVGGPL
30	2533	RKAVTHIN EpCC		2688	NSRGENCG
	2534	KAVTHINS	EpFF	2689	SRGENCGY
	2573	GRKPARI Ep40		2690	RGENCGYR
35	2574	RKPARIIV		2691	GENCGYRR
	2575	KPARLIVF		2692	ENCGYRRC
	2576	PARLIVFP		2693	NCGYRRCR
	2577	ARLIVFPD			
	2578	RLIVFPDL		2707	TSCGNTLI Ep42
40				2721	AACRAAGL ~
				2757	AFTEAMTR
45			Ep43	2758	FTEAMTRY
				2759	TEAMTRYSA
				2760	EAMTRYSA
				2761	AMTRYSA
				2762	MTRYSA
					PP

	2779	DLELIISC Ep44	2878	DLPIIQR Ep47
	2780	LELIISCS	2879	LPIIQRQL
			2880	PPIIQRQLH
			2881	PIIQRHLG
5	Ep45	2794 HDGAGKRV	2882	IIQRHLGL
		2795 DGAGKRVY	2883	IQRHLGLS
		2796 GAGKRVYY	2884	QRLHGLSA
		2797 AGKRVYYL	2885	RLHGLSAF
		2798 GKRVYYLT	2886	LHGLSAFS
10		2799 KRVYYLTR	2887	HGLSAFSL
		2800 RVYYLTRD	2888	GLSAFSLH
		2801 VYYLTRDP	2889	LSAFSLHS
		2802 YYLTRDPT	2890	SAFSLHSY
			2891	AFSLEHSYS
15		2817 WETARHTP	2892	PSLHSYSP
	EpGG	2818 ETARHTPV	2893	SLHSYSPG
		2819 TARHTPVN	2894	LEHSYSPGE
		2820 ARHTPVNS	2895	ESYSPGEI
20		2821 RHTPVNSW		
		2822 HTPVNSWL		
		2823 TPVNSWLG		
		2824 PVNSWLGN		
		2825 VNSWLGINI		
25		2826 NSWLGNII		
		2827 SWLGNIIM		
		2828 WLGNIIIME		
		2829 LGNIIMEA		
		2830 GNIMEAP		
30		2831 NIIMEAPT		
		2832 IIIMEAPTL		
		2833 IMEAPTLW		
		2834 MEAPTLWA		
		2835 EAPTLWAR		
35		2836 APTLWARM		
		2837 PTLWARMI		
		2838 TLWARMIL		
		2839 LWARMILM		
		2840 WARMILMT		
40		2841 ARMILMTH		
		2842 RMILMTHF		
		2843 MILMTHFE		
45		2863 LDCEIYGA Ep46		
		2864 DCEIYGAC		
		2865 CEIYGACY		
		2866 EIYGACYS		
		2867 IYGACYSI		

2912      **LGVPPPLRA** Ep48  
2913      **GVPPLRAW**  
2914      **VPPLRAWR**

5            2938      **AAICGKYL** Ep49  
              2939      **AICGKYLE**  
              2940      **ICGKYLEN**

10          **DLSGWETA**  
**EpHH**

2984      **VSHARPRW** EpII

15          **IV.B.      Differential Assay**

The following assay was performed to distinguish early antigens from later antigens. Antibodies to the early antigens may be detected, and used to diagnose HCV infection more quickly.

Serial bleeds were obtained from a human patient presenting with elevated ALT, but negative for anti-C100-3 antibody. The five bleeds obtained prior to complete seroconversion (C100-3 positive) were pooled and used in the assay at a dilution of 1:2000. The assay was conducted as described in Section IV.A. above. However, one duplicate set of pins was incubated with horseradish peroxidase-labeled goat anti-Human IgG specific antisera, while the other set was incubated with horseradish peroxidase-labeled goat anti-Human IgM specific antisera. Epitopes immunoreactive with IgM antibodies are early epitopes.

The results indicated that most early epitopes are found in the region extending from about amino acid 480 to about amino acid 650. Particularly strong IgM epitopes were octamers beginning with amino acid nos. 506, 510, 523, 553, 562, 580, and the region from 590 to 620. Assays which employ antigens bearing epitopes from this region will permit diagnosis of HCV infection at an early point than assays employing other antigens.

We have additionally tested serial plasma specimens taken from five patients with open heart post-transfusion NANB hepatitis, with studies followed for 3-12 years. Initial bleed dates were less than one week apart. Each specimen was tested for IgG and IgM by EIA against one core antigen (C22), two envelope antigens (E1 and E2), and three nonstructural region antigens (C33c, C100, and

NSS). We found that the IgM response to C22 and C33c preceeded the IgG response for those antigens. NS-5 also induced an IgM response, but this response did not preceed the IgG response for that antigen. Thus, one can prepare assays capable of determining very early stages of infection by utilizing epitopes derived from the C22 and C33c regions and assaying for IgM binding. Antibodies to the C33c region persisted for the longest period of time, suggesting that diagnostic assays directed toward C33c should be the most reliable.

#### IV.C. Sequence Variations in HCV Isolates from Different Individuals

Isolates of HCV which contain sequences which deviate from CDC/HCV1 were identified in human individuals, some of whom were serologically positive for anti-C100-3 antibodies (EC10 was antibody negative). Identification of these new isolates was accomplished by cloning and sequencing segments of the HCV genome which had been amplified by the PCR technique using CDC/HC1 sequences. The method utilizes primers and probes based upon the HCV cDNA sequences described herein. The first step in the method is the synthesis of a cDNA to either the HCV genome, or its replicative intermediate, using reverse transcriptase. After synthesis of the HCV cDNA, and prior to amplification, the RNA in the sample is degraded by techniques known in the art. A designated segment of the HCV cDNA is then amplified by the use of the appropriate primers. The amplified sequences are cloned, and clones containing the amplified sequences are detected by a probe which is complementary to a sequence lying between the primers, but which does not overlap the primers.

IV.C.1. HCV Isolates Isolated from Humans in the U.S.

Blood samples which were used as a source of HCV virions were obtained from the American Red Cross in Charlotte, North Carolina, and from the Community Blood Center of Kansas, Kansas City, Missouri. The samples were screened for antibodies to the HCV C100-3 antigen using an ELISA assay and subjected to supplemental Western blot analysis using a polyclonal goat anti-human HRP to measure anti-HCV antibodies. Two samples, #23 and #27, from the American Red Cross and from the Community Blood Center of Kansas, respectively, were determined to be HCV positive by these assays.

Viral particles present in the serum of these samples were isolated by ultracentrifugation under the conditions described by Bradley *et al.* (1985). RNA was extracted from the particles by digestion with proteinase K and SDS at final concentrations of 10  $\mu$ g/mL proteinase K, and 0.1% SDS; digestion was for 5 1 hour at 37°C. Viral RNA was further purified by extraction with chloroform-phenol.

HCV RNA in the preparation of RNA was reverse transcribed into cDNA. After both strands of the cDNA were synthesized, the resulting cDNA was then amplified by the PCR method. The HCV cDNAs in three clones derived 10 from each HCV isolate, were subjected to sequence analysis. Analysis was essentially by the method described in Chen and Seburg (1985).

Consensus sequences of the clones derived from HCV in samples 23 and 27 are shown in Fig. 3 and Fig. 4, respectively. The variable sequences are also shown in these figures, as are the amino acids encoded in the consensus 15 sequences.

Figures 5 and 6 show comparisons of the aligned positive strand nucleotide sequences (Fig. 5) and putative amino acid sequences (Fig. 6) of samples 23, 27, and HCV1. The amino acid sequence of HCV1 in Fig. 6 represents amino acid numbers 129-467 of the HCV polyprotein encoded by the 20 large ORF in the HCV genomic RNA. An examination of Figs. 5 and 6 show that there are variations in the sequences of the three isolated clones. The sequence variations at the nucleotide level and the amino acid level are summarized in the table immediately below. In the table, the polypeptides designated S and NS1 represent amino acid numbers 130 to ~380, and 380 to ~470, respectively, as 25 those domains were previously known. The numbering is from the putative initiator methionine. The terminology S and NS1 is based upon the positioning of the sequences encoding the polypeptides using the Flavivirus model. As discussed above, however, recent evidence suggests that there is not total correlation between HCV and the Flaviviruses with regard to viral polypeptide domains, 30 particularly in the putative E/NS1 domains. Indeed, HCV polypeptides and their coding domains may exhibit substantial deviation from the Flavivirus model.

Viral particles present in the serum of these samples were isolated by ultracentrifugation under the conditions described by Bradley *et al.* (1985).

RNA was extracted from the particles by digestion with proteinase K and SDS at final concentrations of 10 µg/mL proteinase K, and 0.1% SDS; digestion was for

- 5 1 hour at 37°C. Viral RNA was further purified by extraction with chloroform-phenol.

HCV RNA in the preparation of RNA was reverse transcribed into cDNA. After both strands of the cDNA were synthesized, the resulting cDNA was then amplified by the PCR method. The HCV cDNAs in three clones derived  
10 from each HCV isolate, were subjected to sequence analysis. Analysis was essentially by the method described in Chen and Seenburg (1985).

Consensus sequences of the clones derived from HCV in samples 23 and 27 are shown in Fig. 3 and Fig. 4, respectively. The variable sequences are also shown in these figures, as are the amino acids encoded in the consensus  
15 sequences.

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25 those domains were previously known. The numbering is from the putative initiator methionine. The terminology S and NS1 is based upon the positioning of the sequences encoding the polypeptides using the Flavivirus model. As discussed above, however, recent evidence suggests that there is not total correlation between HCV and the Flaviviruses with regard to viral polypeptide domains,  
30 particularly in the putative E/NS1 domains. Indeed, HCV polypeptides and their coding domains may exhibit substantial deviation from the Flavivirus model.

TABLE:

Sequence Homology

## Nucleotide Encoding Amino Acid Encoded

5	overall			Nucleotide Encoding			Amino Acid Encoded		
	%	S	NS1	overall	%	S	NS1	%	
HCV1/HCV23	93	95	91	92	95	95	87		
HCV1/HCV27	89	93	84	89	95	95	82		
HCV23/HCV27	89	93	85	90	93	93	84		

10            Although there are variations in the newly isolated HCV sequences, the cloned sequences from samples 23 and 27 (called HCV23 and HCV27) each contain 1019 nucleotides, indicating a lack of deletion and addition mutants in this region in the selected clones. The sequences in Figs. 5 and 6 also show that the isolated sequences are not rearranged in this region.

15            A comparison of the consensus sequences for HCV1 and for the other isolates of HCV is summarized in the Table, *supra*. The sequence variations between the chimpanzee isolate HCV1, and the HCVs isolated from humans are about the same as that seen between the HCVs of human origin.

20            It is of interest that the sequence variations in two of the putative domains is not uniform. The sequence in a putative S region appears to be relatively constant, and randomly scattered throughout the region. In contrast, a putative NS1 region has a higher degree of variability than the overall sequence, and the variation appears to be in a hypervariable pocket of about 28 amino acids which is located about 70 amino acids downstream from the putative N-terminus  
25            of the putative polyprotein.

Although it may be argued that the detected variations were introduced during the amplification process, it is unlikely that all of the variations are from this result. It has been estimated that Taq polymerase introduces errors into a sequence at approximately one base per 10 kilobases of DNA template per cycle (Saiki *et al.* (1988)). Based upon this estimate, up to 7 errors may have been introduced during the PCR amplification of the 1019 bp DNA fragment. However, the three subclones of HCV-23 and HCV-27 yielded 29 and 14 base variations, respectively. The following suggest that these variations are naturally

occurring. About 60% of the base changes are silent mutations which do not change the amino acid sequence. Variations introduced by the Taq polymerase during PCR amplification would be expected to occur randomly; however, the results show that the variant sequences are clustered in at least one specific region.

5

#### IV.C.2. HCV Isolates from Humans in Italy and in the U.S.

Segments of HCV RNA present in different isolates were amplified by the HCV/cPCR method. These segments span a region of ~0.6 Kb to ~1.6 Kb downstream from the methionine encoding start codon of the putative HCV polyprotein. The isolates are from biological specimens obtained from HCV infected individuals. More specifically, isolate HCT #18 is from human plasma from an individual in the U.S.A., EC1 and EC10 are from a liver biopsy of an Italian patient, and Th is from a peripheral blood mononucleocyte fraction of an American patient. Comparable segments of HCV RNA have been isolated from a chimpanzee.

RNA was extracted from the human plasma specimens using phenol:CHCl<sub>3</sub>:isoamyl alcohol extraction. Either 0.1 mL or 0.01 mL of plasma was diluted to a final volume of 1.0 mL, with a TENB/proteinase K/SDS solution (0.05 M Tris-HCl, pH 8.0, 0.001 M EDTA, 0.1 M NaCl, 1 mg/mL Proteinase K, and 0.5% SDS) containing 10 to 40 µg/mL polyadenylic acid, and incubated at 37°C for 60 minutes. After this proteinase K digestion, the resultant plasma fractions were deproteinized by extraction with TE (50 mM Tris-HCl, pH 8.0, 1 mM EDTA) saturated phenol, pH 6.5. The phenol phase was separated by centrifugation, and was reextracted with TENB containing 0.1% SDS. The resulting aqueous phases from each extraction were pooled, and extracted twice with an equal volume of phenol/chloroform/isoamyl alcohol [1:1(99:1)], and then twice with an equal volume of a 99:1 mixture of chloroform/isoamyl alcohol. Following phase separation by centrifugation, the aqueous phase was brought to a final concentration of 0.2 M Na acetate, and the nucleic acids were precipitated by the addition of two volumes of ethanol. The precipitated nucleic acids were recovered by ultracentrifugation in a SW 41 rotor at 38 K, for 60 minutes at 4°C or in a microfuge for 10 minutes at 10 K, 4°C.

RNA extracted from the liver biopsy was provided by Dr. F. Bonino, Ospedale Maggiore di S. Giovanni Battista, Torino, Italy. The mononucleocyte fraction was obtained by sedimentation of the individual's aliquot of blood through Ficoll-Paque® (Pharmacia Corp), using the manufacturer's directions. Total RNA was extracted from the fraction using the guanidinium thiocyanate procedure described in Choo et al (1989).

- Synthesis of HCV cDNA from the samples was accomplished using reverse transcriptase. Following ethanol precipitation, the precipitated RNA or nucleic acid fraction was dried, and resuspended in DEPC treated distilled water.
- 5      Secondary structures in the nucleic acids were disrupted by heating at 65°C for 10 minutes, and the samples were immediately cooled on ice. cDNA was synthesized using 1 to 3 µg of total RNA from liver, or from nucleic acids (or RNA) extracted from 10 to 100 µL of plasma. The synthesis utilized reverse transcriptase, and was in a 25 µL reaction, using the protocol specified by the manufacturer, BRL.
- 10     All reaction mixtures for cDNA synthesis contained 23 units of the RNAase inhibitor, Rnasin® (Fisher/Promega). Following cDNA synthesis, the reaction mixtures were diluted with water, boiled for 10 minutes, and quickly chilled on ice.
- 15

Each set of samples was subjected to two rounds of PCR amplification. The primers for the reactions were selected to amplify regions designated "EnvL" and EnvR". The "EnvL" region encompasses nucleotides 669-1243, and putative amino acids 117 to 308; the "EnvR" region encompasses nucleotides 1215-1629, and encodes putative amino acids 300-408 (the putative amino acids are numbered starting from the putative methionine initiation codon).

20     The PCR reactions were performed essentially according to the manufacturer's directions (Cetus-Perkin-Elmer), except for the addition of 1 µg of RNase A. The reactions were carried out in a final volume of 100 µL . The PCR was performed for 30 cycles, utilizing a regimen of 94°C (1 min), 37°C (2 min), and 72°C (3 min), with a 7 minute extension at 72°C for the last cycle. The 25 samples were then extracted with phenol:CHCl<sub>3</sub>, ethanol precipitated two times, resuspended in 10 mM Tris HCl, pH 8.0, and concentrated using Centricon-30 (Amicon) filtration. This procedure efficiently removes oligonucleotides less than

30 nucleotides in size; thus, the primers from the first round of PCR amplification are removed.

The Centricon-30 concentrated samples were then subjected to a second round of PCR amplification. Amplification by PCR was for 35 cycles 5 utilizing a regimen of 94°C (1 min), 60°C (1 min), and 72°C (2 min), with a 7 minute extension at 72°C for the last cycle. The samples were then extracted with phenol:CHCl<sub>3</sub>, precipitated two times, and digested with EcoRI. The PCR reaction products were analyzed by separation of the products by electrophoresis on 6% polyacrylamide gels. DNA of approximately the estimated size of the 10 expected PCR product was electroeluted from the gels, and subcloned into either a pGEM-4 plasmid vector or into λgt11. The expected product sizes for the EnvL and EnvR after the first round of amplification are 615 bp and 683 bp, respectively; after the second round of amplification the expected product sizes for EnvL and EnvR are 414 bp and 575 bp, respectively. The plasmids containing the 15 amplified products were used to transform host cells; the pGEM-4 plasmid was used to transform DH5-alpha, and λgt11 was used to transform C600 delta-HFL. Clones of the transformed cells which either hybridized to the appropriate HCV probes, or those which had inserts of the correct size were selected. The inserts were then cloned in M13 and sequenced. The probes for all of the HCV/cPCR products consisted of <sup>32</sup>P labeled sections of HCV cDNA which had been prepared by PCR amplification. 20

Sequence information on variants in the EnvL region was obtained from 3 clones from HCT #18, 2 clones from TH, 3 clones from EC1, and from the HCV1 clones. A comparison of the composite nucleotide sequence of each 25 isolate derived from these clones is shown in Fig. 7. In the figure, each sequence is shown 5' to 3' for the sense strand for the EnvL region, and the sequences have been aligned. The vertical lines and capital letters indicate sequence homology, the absence of a line and an uncapitalized letter indicates a lack of homology. The sequences shown in the lines are as follows: line 1, Thorn; line 2, EC1; line 3, HCT #18; line 4, HCV1. 30

Sequence information on variants in the EnvR region was obtained from two clones of EC10, and from HCV1 clones. The two EC10 clones differed by only one nucleotide. A comparison of the nucleotide sequences of EC10(clone

2) and a composite of the HCV1 sequences is shown in Fig. 8; each sequence is shown 5' to 3' for the sense strand of the EnvR region, and the sequences have been aligned. The double dots between the sequences indicate sequence homology.

5 A comparison of the amino acid sequences encoded in the EnvL (amino acids #117-308) and EnvR region (amino acids #300-438) for each of the isolates is shown in Fig. 9 and Fig. 10, respectively. Included in the Figures are sequences for the isolates JH23 and JH27, described above. Also indicated are sequences from a Japanese isolate; these sequences were provided by Dr. T. Miyamura, Japan. In the figures, the amino acid sequence for the region is given in its entirety for HCV1, and the non-homologous amino acids in the various isolates are indicated.

10 As seen in Fig. 9, In the EnvL region there is overall about a 93% homology between HCV1 and the other isolates. HCT18, Th, and EC1 have about a 97% homology with HCV1; JH23 and JH27 have about 96% and about 15 95% homology, respectively, with HCV1. Fig. 10 shows that the homologies in the EnvR region are significantly less than in the EnvL region; moreover, one subregion appears to be hypervariable (*i.e.*, from amino acid 383-405). This data is summarized in the Table immediately below.

20 Table: Homology of EnvR Region

Isolate	Percent Homology with HCV1		
	AA330-AA438	AA383-AA405	
JH23(U.S.)	83	57	
JH27(U.S.)	80	39	
25 Japanese	73	48	
EC10 (Italy)	84	48	

VI. Industrial Applicability

30 The epitopes identified herein can be used to make polypeptide products as described above for applications such as the screening of blood for HCV infection, clinical HCV diagnosis, the generation of antibodies, and preparation of medicaments. Other applications are described above, and still others will be readily apparent to those of ordinary skill.

## VII.

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- U.S. Patent No. 4,444,887    U.S. Patent No. 4,493,890
- U.S. Patent No. 4,816,467

WHAT IS CLAIMED:

1. A polypeptide comprising a truncated HCV sequence containing an HCV epitope of the formula

5

aa<sub>x</sub>-aa<sub>y</sub>

wherein aa denotes an amino acid;

x and y are integers such that y-x ≥ 6;

aa<sub>x</sub>-aa<sub>y</sub> indicates a portion of the amino acid sequence of Figure 1; and x is selected from the group consisting of 23-34, 36, 66-79, 81-94, 96-

10 98, 101-103, 186-189, 191, 206, 223, 232, 256, 286, 297-299, 321, 347, 357, 413, 414, 432, 465-471, 480-484, 501, 502, 521, 540-549, 579, 594-599, 601-613, 641, 662-665, 685, 705, 706, 729, 782-789, 801, 851-855, 893, 916, 928, 946, 952-954, 1026, 1072, 1109, 1112-1117, 1218, 1240, 1280-1285, 1322, 1338, 1371, 1384, 1410, 1411, 1454, 1492, 1493, 1532-1535, 1560, 1561, 1566-1568, 15 1571-1577, 1601-1607, 1615-1620, 1655, 1695, 1710-1712, 1728, 1729, 1758-1762, 1781, 1808, 1821, 1851, 1880, 1908-1913, 1925, 1940-1948, 1951, 1966-1969, 1999, 2001-2004, 2006-2014, 2024, 2048-2053, 2055-2057, 2071, 2088-2093, 2108, 2122-2148, 2165, 2187, 2226-2232, 2244-2249, 2267, 2281-2286, 2288, 2289, 2325-2327, 2346, 2347, 2349, 2382, 2401, 2417-2422, 2439-2444, 20 2446-2456, 2469, 2471-2476, 2495, 2533, 2534, 2573-2578, 2602-2604, 2606-2612, 2632-2638, 2660, 2676-2679, 2688-2693, 2707, 2721, 2757-2762, 2779, 2794, 2795, 2797-2799, 2801, 2802, 2817-2843, 2863-2867, 2878-2884, 2886-2895.

25

2. The polypeptide of claim 1 which is about 100 amino acids or less in length.

3. The polypeptide of claim 2 wherein y-x ≤ 50.

30

4. The polypeptide of claim 2 wherein y-x ≤ 20.

5. The polypeptide of claim 2 wherein y-x < 10.

6. The polypeptide of claim 2 wherein x is selected from the group consisting of 506, 510, 523, 553, 562, 580, and 590-620.

7. A polypeptide of about 100 amino acids or less comprising an HCV epitope of the formula

$\text{aa}_x\text{-aa}_y$

wherein aa denotes an amino acid;

x and y are integers such that  $y-x \geq 6$ ;

aa<sub>x</sub>-aa<sub>y</sub> indicates a portion of the amino acid sequence of Figure 1; and  
10 x is selected from the group consisting of 35 (where y is less than 45),  
80 (where y is less than 90), 95 (where y is less than 110), 99 (where y is less  
than 120), 100 (where y is less than 150), 190 (where y is less than 210), 500  
(where y is less than 550), 600 (where y is less than 625), 1260 (where y is less  
than 1280), 1569 (where y is less than 1931), 1570 (where y is less than 1590),  
15 1694 (where y is less than 1735), 1949 (where y is less than 2124), 1950 (where y  
is less than 1985), 2000 (where y is less than 2050), 2005 (where y is less than  
2025), 2054 (where y is less than 2223), 2250 (where y is less than 2330), 2287  
(where y is less than 2385), 2290 (where y is less than 2310), 2345 (where y is  
less than 2375), 2348 (where y is less than 2464), 2445 (where y is less than  
2475), 2470 (where y is less than 2490), 2605 (where y is less than 2620), 2780  
20 (where y is less than 2830), 2796 (where y is less than 2886), 2800 (where y is  
less than 2850), and 2885 (where y is less than 2905).

8. An immunoassay reagent comprising a polypeptide according to  
25 any of claims 1-7.

9. The immunoassay reagent of claim 8 wherein  $y-x \leq 50$ .

10. The immunoassay reagent of claim 8 wherein x is selected from  
30 the group consisting of 506, 510, 523, 553, 562, 580, and 590-620.

11. A method for detecting the presence of antibodies immunoreactive with Hepatitis C virus (HCV) proteins in a sample, said method comprising:  
contacting an immobilized immunoassay reagent according to claim 8  
with said sample; and  
5 detecting antibodies bound to said reagent.

12. A method for inducing an immunological response in a subject against HCV, said method comprising:

10 administering to said subject an effective amount of a polypeptide according to any one of claims 1-7.

13. A composition for inducing an immunological response in a subject against HCV, said composition comprising an effective amount of a 15 polypeptide according to any one of claims 1-7.

14. A monoclonal or polyclonal antibody composition wherein said antibodies bind the HCV epitope of a polypeptide according to claim 1.

20 15. A method of making a polypeptide according to any of claims 1-7 wherein said polypeptide is prepared by recombinant expression or chemical synthesis.

## FIG. I - I

R T

MSTNPKPQKKNRNTNRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR  
 KTSERSQPRGRRQPPIPKARRPEGRTWAOPGYPWPLYGNECGGWAGWLLSP-100  
 RGSRPSWGPTDPRRRSRNLGVIDTLTCGFADLMGYIPLVGAPLGGAAARA.

T

LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL-200  
 YHVTNDPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRD  
 GKLPATQLRRHIDLIVGSATLCSALYVGDLGSVFLVGQLFTFSPRRHWT-300

V

TQGCNCISIYPGHITGHRMAWDMMMNWSPTTALVMAQLLRIPQAILEDIAAG  
 AHWGVLAGIAYFSMVGNWAKVLVVLLFAFGVDAETHVTGGSAGHTVSGFV-400  
 SLLAPGAQNQVQLINTNGSWHLNSTALNCNSLNTGWLALFYHHKFNSS  
 GCPERLASCRPLTDFDQGWGPISYANGSPDQRPYCWHYPPKPCGIVPAK-500  
 SVCGPVYCFTPSPVVVGTTDRSGAPTYSWGENDTDVFVLNNTRPPLGNWF  
 GCTWMNSTGFTKVCVGAPPVCIGGAGNNTLHCPTDCFRKHPDATYSRCGSG-600

I

PWLTPRCLVDYPYRLWHYPCTINYTIKFIRMYVGGVEHRLEAACNWTRGE  
 RCDLEDRDRSELSPLLTTTQWQVLPCSFTTLPALSTGLIHLHQNIVDVQ-700  
 YLYGVGSSIASWAIKWEYVVLLFLLLADARVCSCILWMMLLISQAEAALEN  
 LVILNAASLAGTHGLVSFLVFFCFAWYLKWKWVPGAVYTFYGMWPLLLL-800

(N)

LALPORAYALDTEVAASC GG VVLVGLMALTLS PYYKRYISWCLWWLQYFL  
 TRVEAQLHVWIPLNVRGGRAVILLMC AVHPTLVFDITKL LLA VFGPLW-900  
 ILQASLLKVPYFVRVQGLLRFCALARKMIGGHYVQMVIIKLGALTGTYVY  
 NHLTPLRDWAHNGLRLDAVAVEPVVFSQMETKLITWGADTAACGDIINGL-1000  
 PVSARRGREILLGPADGMVSKGWRL LAPITAYAQQT RGLLGCII TSLTGR  
 DKNQVEGEVQIVSTAATFLATCINGVCWTYHGAGTRTIASPKG PVIQM-1100

S T

YT NVDQDLV GWPAPQGSRS LTPCTGSSDLYLVTRHADVIPVRRRGDSRG  
 SLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEN-1200  
 LETTMRSPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYK

L

VLVLNPSVAATLGFGAYMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFL-1300

ADGGCGSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATAT  
 PPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKC-1400  
 DELAAKLVALGINAVAYYRGLDVSIPTSGDVVVVATDALMTGYTGDFDS

Y (S)

V IDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRTQR GRG RTGRG KPGIYR-1500  
 FVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPV  
 CQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENLPYLVAYQATVCARAQAP-1600  
 PPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEITLTHPVTKYIMTCMS  
 ADLEVVTSWVLVGGVIAALAAYCLSTGCVVIVGRVVL SGKPAIIPDREV-1700  
 LYREFDEMEEC SQHLPYIEQGMM LAEQFKQKALG LLQTASRQAEVIA PAV  
 QTNWQKLET FWAKHMWNFISGIQYLAGLSTLPGNP AIASLMAFTAATVSP-1800  
 LTTSQTL LFNI LG GWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLI D

(G)

I LAGY GAGVAG ALVAPKIMSGEV P STEDLVNLLPAILSPGALVVGVVCAA-1900

(HC)

I LRRHVGPGEGAVQWMNRLIAFASRGNHVSP THY VPESDAAARV TAILSS

### FIG. I - 2

LTVTQLLRRRLHQWISSECTTPCSGSWLRIWDWICEVLSDFKTWLKAKLM-2000

(V)

PQLPGIPFVSCQRGYKGWWRGDGIMHTRCHGAEITGHVKNGTMRIVGPR  
 TCRNMWSGTFPINAYTTGPCTPLPAPNYTFALWRVSAEEYVEIROVGDFH-2100  
 YVTGMTTDNLKCPCQVPSPEFFTELDGVRLHRFAPPCKPLLREEVSFRVG  
 LHEYPVGSQLPCEPEPDVAVLTSMLDPSHITAEEAGRRLARGSPPSVAS-2200  
 SSASOLSQLSAPSLKATCTANHDSPDAELIEANLLWRQEMGGNITRVESENKV  
 VILDSFDPLVAEEDEREISVPAEILRKSRFAQALPVWARPDPPLVET-2300

(S)

WKKPDYEPPVVHGCPLPPPSSPPVPPPRKKRTVVLTESTLSTALAELATR

(FA)

SFGSSSTSGITGDNTTSSEPAKPGCPPSDAESYSSMPPLEGEPGDPDL-2400  
 SDGSWSTVSSEANAEDVVCCSMSYSWTGALVTPCAAEEQKLPINALNSL  
 LRHHNLVYSTTSRSACQRQKKVTFDRLQVLDHYQDVLKEVKAASKVKA-2500

(F)

NLLSVEEACSLTPPHSAKSFKGYGAKDVRCHARAKAVTHINSVWKDLLEDN  
 VTPIDTTIMAKNEVFCVQPEKGRKPARLIVFPDLGVRVCEKMALYDVVT-2600  
 KLPLAVMGSSYGFQYSPGQRVEFLVQAWSKKTPMGFSYDTRCFDSTVTE

(G)

SDIRTEEAIYQCCDLDPOARVAIKSLTERLYVGGPLTNSRGENCYRRCR-2700  
 ASGVLTTSCGNLTTCYIKARAACRAAGLQDCTMLVCGDDLVVICESAGVQ  
 EDAASLRATEAMTRYSAPPGDPQQPEYDLELITSCSSNVSAHDGAGKR-2800  
 VYYLTRDPTTPLARAATWHTPVNSWLGNIIMFAPTLWARMILMTHFF  
 SVLIARDOLEQALDCEIYGACYSIEPLDLPPIIQRLHGLSAFSLHSYSPG-2900

G

EINRVAACLRKLGVPLRAWRHRARSVRARILLARGGRAAICGKYLFNWAV

(P)

RTKLKLTPIAAAGQDLSGWFTAGYSGGDIYHSVSHARPRWIWFCLLLL-3000  
 AGVGIYLLPNRO-3011

Stop codon

( ) - Heterogeneity due possibly  
 to 5' or 3' terminal cloning  
 artefact.

FIG. I-3

SUBSTITUTE SHEET

FIG.2-1

5' terminus-----

```

CACTCCACCATGAAATCACTCCCCTGTAGGGAACTACTGTCTTCACGCCAGAACCGGTCTAG
CCATGGCGTTAGTATGAGTGTCTGGCAGCCCTCCAGGACCCCCCTCCGGGAGAGCCATA
GGGGTCTGGGAACCGGTGAGTACACCGGAATTGGCCAGGACGACCGGGTCTTCTTGGA
TCAACCCGCTCAATGGCCTGGAGATTGGCGTCCCCGGAAAGACTGCTAGGCCAGTAGT
GTGGGTTGGAAAGGGCTTGTTACTGCCGTGATAAGGGTGTGCGAGTGGCCAGTGGGGAG-300

```

(Putative Initiator methionine codon)

```

GCTCTAGACCCTGCACCATGAGCACGAAATCCTAAACCTCAAAAAAAACAAACGTAAC
CACCAACCCGTCGGCCACAGGACGTCAAGTTCGGGGTGGGGTCAAGTCGATCGTTGGGAGT
TTACTGTTGGCGCAGGGCCCTAGATGGGTGTTGGCTAGGCTATCCCAAGGCTCGTGGCCCAGGGCAG
GGGGTCTGCAACCTCGAGGGTAGACGCTCAGGCTACCCCTGGCCCTCTATGGCAATGGCAATGGGCTGCGGGTGGGC-600
GACCTGGCTCAGGGGGTACCCCTGGCCCTCTGGGCTCTGGGCTAGCTGGGGCTACGTCGGGCTTCGGCCACCTCAT
GGGATGGCTCTGTCCTGGGCAATTGGGTAAGGTCAATGATAACCTTACGTCGGGCTGGGCTGGGCAATGG
TAGGTGGCAATTGGGCAATTGGGTAAGGTCAATGATAACCTTACGTCGGGCTGGGCTGGGCAATGG
GGGTACATACCGCTCGTGGGGCCCTCTGGAGGGCTGGGCTGGGCAACTATGCAACAGGGAAACCTTCTGGTGTCTT
GGTCCGGTTCTGGAAAGACGGGGTGAACATGCAACAGGGAAACCTTCTGGTGTCTT

```

C

```

CTCTATCTCCTCTGGCCCTGCTCTTGACTTGCCCTACCCATTGGCCCTACCAAGT-900
GGCAACTCCAAGGGCTTACACAGTCACCAATGATGCCCTAACCTCGAGTATTGGTA
CGAGGGGGGAGTGCCATCCTGCACACTCCTGGGGTGGGATGACCCCTACGGTGGCCACAGGATGGCAAACCTCCC
CCCTCGAGGTGGGGGATGACGGTCACTCGATCTGGGGGAGGGCCACCCCTCTGGGG
GGGAGGCTTCGAGGTCAATCGATCTGGGGGAGGGGAGGGGAGGGGAGGGGAGGGG
CCTCTACGTGGGGACCTATGGGGCTGTCTTCTGGGGCAACTGTTCACCTCTC-1200
TCCCAGGGCCACTGGACGCAAGGTGCAATTGCTATCTGGGGCATATAAC

```

## **SUBSTITUTE SHEET**

**FIG.2 - 3**

```

ACGGCAACTGCACTGTGGATTCCCCCTCAACGTCGGAGGGGGCGACCCGCTCAT
CTTACTCATGTGTGCTGTACACCCGACTCTGGTATTGACATCACCAAATGCTGGC- 3000
CGTCTTGGGACCCCTTGGATTCTCAAGGCCAGTTGCTTAAGTACCTACTTTGTGCG
CGTCCAAGGGCCTTCCGGTTCTGGGGCTTAGGGGGAAAGATCGGAGGCCATTACG
GCAAATGGTCATCATTAAAGTTAGGGGGCACAAACGGCTTGCGAGATCTGGCGTGGCTAGGCCAGT
TCCCTTCGGGACTGGGCACAAACGGCTTGCGAGATCTGGCGTGGCTAGGCCAGT
CGTCTTCCCAAAATGGAGACCAAGCTCATACGTGGGGCAATAACGCCGGTGGCG- 3100
TGACATCATCAACGGCTTGGCTTGGGGAGGATACTGCTGGGCC
AGCCGATGGAATGGTCTCCAGGGCTCCTAGGGTGCATAATACCGGCTAACCTGGGGACA
GCAGACAAGGGCTCCTAGGGTGCAGATTGTGTCACACTGGTCCAGGCTTGCCAAACCTGGCAACGGTGCAT
ACTGGAGGGTGAAGTCCAGATTGTGTCACACTGGTCCAGGCTTGCCAAACGGGACCATGGGTACCCAA- 3600

```

T  
GGTCCTGTCAATCAGATGATAACCAATGAGACCTGTGGCTGGCCGGCTC

C  
GCAAGGTAGCCGCTCATTTGACACCCCTGCACTTGGGGCTCCTGGACCTTACCTGGTCAC
GAGGCAAGGGGATGTCATTCCCCTGGCTGCGGGGGGCTGATAAGCAGGGCAGCCTGGCTGTC
GCCCGGGCCATTCTACTTCTGAAAGGCTCCCTGGGGGCTGGCTGTTGCCCCGGGG
GCACGCCGTGGCATATTAGGGCCGGTGTGCACCGGGGGTGGCTAAGGGGGTGGA- 3900
CTTATCCTGTGAGAACCATAGAGAACCAACCCTGAGGTCCCCGGGTGGTTACGGATAACTC
CTCTCCACCAAGGTGGCTCACCTCCAGGGCTTCCAGGTGGCTAACCTCCACAGGGCAG
GGCAAAAGCACCAAGGTGGCTGCAATGGCAGGTGGCTATAAGGGCTAGTACT
CAACCCCTCTGGCTGCAACACTGGGTTACATGGCTTACATGGTCCAAGGGCTATGGGAT

T  
CGATCCTAACATAGGACCCGGGTGAGAACAAATTACCACTGGCAGCCCCATCACGGTACTC- 4200
CACCTACGGCAAGTTCCCTGGCGACGGGGGGTGGCTGGGGGGCTTATGACATAATAAT
TTGTGACGAGTGCACCTCCACGGATGGCCACATCCATCTGGCATGGGACTGTCCTTGA
CCAAGCAAGAGACTGGGGGGAGACTGGTGTGCTGGCCACCGCCACCCCCCTCGGGGTC
CGTCACTGTGCCCATCCCCAACATCGAGGGGGTGGCTGTCCACCCGGAGAGATCCC
TTTTAACGGCAAGGCTATCCCCCTGGAAGTAATCAAGGGGGAGACATCTCATCTTCTG- 4500
TCATTCAAAAGAACGAAACTGGCGACGAACTGGCGCAAGGCTGGCATGGGATCAATGC
CGTGGCCCTACTACGGGGTCTTGTGACGTTGTCGCGTCAATCCCGACAGGGGATGGTGTGCGT

## **SUBSTITUTE SHEET**

FIG. 2-5

## **SUBSTITUTE SHEET**

FIG. 2-6

## **SUBSTITUTE SHEET**

TAGCCAGGTCTCGTCTCATCGTGGCTCCCGATCTGGCGCTGGCGAAAGATGGC-8100  
 TTGTAACGACGTTACANAGCTCCCTTGCCCCGTGATGGAAAGCTCCTACGGATTCCA  
 ATACTCACAGGACAGGGTTGAATTCCCTCGTGCAGCGTGGAAAGTCCAAAGAAAACCCC  
 AAATGGGTTCTCGTATGATAACCCGGCTGGCTTGACTCCACAGTCACGAGGGACATCCG  
 TACGGAGGAGGCAATTCTACCAATGTTGACCTCGACCCCCAAGGCCGGTGGCATCAA  
 GTCCCTCACCGAGGGCTTTATGTTGGGCCCTTACCAATTCAAGGGGGAGAAGCTG-8400  
 CGGCTATCCAGGTGCGGCCGAGGGCTACTGACAACTAGCTGTGGTAACACCCCTCAC  
 TTGCTACATCAAGGCCGGCAGGCCCTGTCGAGGCCGAGGGCTCAGGACTGACCATGCT  
 CGTGTGCGGAGCAGACTTAGTCTGTATCTGTGAAAGGGGGGAGGAGGGACGGGC  
 GAGCCTGAGAGGCTTACGGGGCTATGACCAGGTATAACATCATGGCTCAAACT  
 ACAACAGAAATACGACTTGGAGGCTATAACATCATGGCTTACCCGTGACCCCTAAC  
 CGACGGCTGGAAAGAGGGTCTACTACCTCACCGTACATGGCTAACACCCCCCTCGCGAG  
 AGCTGGCTGGAGACAGCAAGACACACTCCAGTCAATTCTGGCTAGGCACAAATAATCAT  
 GTTGGCCCCACACTGTGGGAGGATGATACTGATGACCCATTCTTAGGCTCCTTAT  
 ACCCAGGGACCGCTGAACAGGGCCCTCGATGGAGATCTACGGCTACTCCAT  
 AGAACCACTTGATCTACCTCAATCAAAAGACTCCATGGCCTAGGGCATTTCACT-9000  
 CCACAGTTACTCTCAGGTGAAATTATAGGGTGGCCATGCTCAGAAAACCTGGGGT

G  
ACCGCCCTTGGAGCTGGAGACACCGGGCCGGAGGCTCCGCCCTAGGCTTCTGGCCAG  
AGGAGGCAGGGCTGCCATATGGCAAGTACCTCTTCAACTGGCAGTAAGAACAAAGCT  
CAAACCTACTCCAATTAGGGGGCTGGCCAGCTGGACTTGTCCGGCTTGCTGCTGG  
CTACAGGGGGAGACATTATCACAGCGTGTCTCATGCCGGCCCCGCTGGATCTGGTT-9300  
TTCGCTACTCCTGGCTGAGGGTAGGCATCTACTCCTCCCCAACCGATGAAGGTT  
GGGTAAACACTCCGGCCT-----3' terminus

Some clonal heterogeneities producing amino acid substitutions are shown. There are many other "silent" mutations (not shown).

Human 23

FIG. 3-2

TYR Pro GLY His Ile Thr GLY His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro  
 TAT CCC GGC AT ATA ACC GG T CAC CG C AT TGG C AT TGG G AT AT G A A C T G G T C C C T  
 G  
 Thr Ala Ala Leu Val Val Ala Glu Ile Leu Arg Ile Pro Glu Ala Ile Leu Asp Met Ile  
 ACG GGG C AT TGG C AT TGG C AT TAG G C T CAG G C T C C G AT CCC C A C A A G C C A T C G A C T G A C  
 G  
 A Ia GLY Ala H1 S Tr P G1 Y Val Leu Ia GLY Met Ala Ty r Phe Ser Met Val GLY Asn TrP  
 GCT GGT GCT CACT TGG GAG TCC TGG GAT TGG GAT TGG C AT TGG C AT TGG C AT TGG G A A C T G G  
 G  
 Ala Lys Val Leu Val Leu Phe Ala GLY Val AlA SP ALA GLU Thr H1 S Arg Thr  
 GCG AAG GT C CT GG T ACT GCT GCT TCT ATT G C C G G T C G A C G G G A A A C C A C C G T A C C  
 G  
 GLY GLY Ser Ala Ala Arg Ser Thr Ala GLY Val Ala Ser Leu Phe Thr Pro GLY Ala Arg  
 GGG GAA AGT G C C G C C G C A C G C T G G A G T T G C T A G T C T C A C A C C A G G C G C T A G G  
 C  
 C  
 Glu Asn Ile Glu Ile Asn Thr Asn GLy Ser Trp His Ile Asn Ser Thr Ala Leu Asn  
 CAG AAC AT CCAG CT GAT CA AC ACC AA C  
 AT  
 Cys Asn Asp Ser Leu Thr Gly Trp Leu Ala GLY Val Phe Tyr H1 S Lys Phe Asn  
 TGCA AT GAC CAG CCT TAC C ACC C G G C T G G C T A G C G C A T T C A C C A T A A T C A A C  
 A  
 Ser Ser GLY Cys Pro GLY Ile Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Ala Gln  
 TCT TCAG G G C T G T C C C G A G G G T T G C C A G C T G C C A G C T G C C C T C A C C G A T T T G C C C A G G  
 G  
 A  
 G  
 A

FIG. 4-1 Human 27

GlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAla  
 1 GGCTTCGCCGACCTCATGGGTACATTCCGGCTCGTCGGCTCTGGGGCTTGCCC  
 ARGAlaLeuAlaHisGlyValArgValLeuGlwaspGlyValAsnTyrAlaThrGlyAsn  
 61 AGGGCCCTGGCCATGGGCTCCGGTTCTGGAAAGACGGCGTGAACATGCAACAGGGAAC  
 LeuProGlyCysSerPheSerIlePheLeuAlaLeuLeuSerCysLeuThrValPro  
 121 CTTCCCTGGTTGCTCTTCTATCTTCTCCTACACTTCCTGCCTCTGCCTTGACCCGTGCC  
 AlaSerAlaTyrglvalAlaAsnSerSerGlyIleTerHisValThrAsnAspCysPro  
 181 GCATGGCCTACCAAGTAGCCAACCTGGCAACTCCTGGGCAATTACCAATGTCACCAATGATGCCCC  
 AsnSerIleValTyrGluThrAlaAspThrIleLeuHisSerProGlyCysValPro  
 241 AATTGAGTATTGTTACGAGACGGCCGACACCATCCTACACTTCCTGCCTGCTGCCCT  
 C  
 CysValArgGluGlyAsnAlaSerLysCystePvalProValAlaProThrValAlaThr  
 301 TGGCTTCGGGGTAACGGCTCGGAAATGTTGGGTGGCTAGCCCCCACAGTGGCCACC  
 G  
 ArgAspGlyAsnLeuProAlaThrGlnLeuIargArgHisIleAspLeuValGlySer  
 361 AGGGACGGCAACCTCCCCGCAACGGAGCTCGACGTCACTCGATCTGCTGTGGGAGT  
 G  
 G  
 AlaThrLeuCysSerAlaLeuTyrValGlyAspLeuCysGlySerValPheLeuValGly  
 421 GCCACCCCTTGCTGGCCCTATGTCGGGACTGTGCGGGTCTGTCTTGTGCTGCTGGT  
 C  
 GlnLeuPheThrPheSerProArgArgHisIlePheSerIleAspCysAsnCysSerIle  
 481 CAACTGTTCACTTCTCCCCAGGGCCACTGGACAAACGCAAGATTGCAACTGCTCTATC  
 A

## FIG. 4-2

Tyr Pro Gly His Ile Thr Gly Ile Val Leu Asp Met Ala Thr Asp Phe Met Met Asn Trp Ser Pro  
 TACCCGGCATATAACGGACACGGCATGGATATGATGAACTGGTCCCCCT  
 Thr Ala Ala Leu Val Met Ala Gln Leu Ile Arg Ile Pro Gln Ala Ile Leu Asp Met Ile  
 ACAGCAGCGCTGGTAATGGCTCAAGCTCAGTCAGGATCCCAGCAAGGCCATCTGGACATGATGAC  
 G

Ala Ala Gly Ala His Trp Glu Val Leu Ala Gly Ile Ala Ile Tyr Phe Ser Met Val Gly Asn Trp  
 GCTGGTGCTCACTGGGAGTCCTAGGGCATAGCGTATTCTCCATGGTGGGAACCTGG  
 Ala Lys Val Leu Val Leu Ile Phe Ala Gly Val Ala Spal a Thr Thr Thr Tyr Thr Thr  
 GCGAAGCTCCTGGTGGCTGCTGTTGCCGGGTGGATGGACAAACCTAACCC  
 Gly Gly Asn Ala Ala Arg Thr Thr Glu Ala Leu Thr Ser Phe Phe Ser Pro Gly Ala Lys  
 GGGGGAAATGGCTGCCAGGACCACGCAAGGGCTCACCAAGTTTCAGGCCAGGCCAAG  
 Gln Asp Ile Gln Ile Asn Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn  
 CAGGATATCCAGGTGATCAACACCAAACGGCAGTGGCACATCAATCGCACGGCCTTGAAAC  
 G

Cys Asn Ala Ser Leu Asp Thr Gly Trp Val Ala Gly Ile Phe Tyr Tyr His Lys Phe Asn  
 TGTAAATGCCAGGCCTCGACACTGGCTGGGTRAGGCCAGCTGTCTTCTATTACCAAAATTCAAC  
 T

Ser Ser Gly Cys Pro Glu Arg Met Ala Ser Cys Arg Pro Leu Ala Asp Phe Asp Gln  
 TCTTCAGGCTGCCCGAGAGGATGGCTAGGCCAGCTGTCTTCTATTACCAAAATTCAAC  
 C

FIG. 5-1

1. human 27 2. HCV 1 3. human 23

1 CGGCTTCGGCGACCTCATGGGTACATCCGCTCGTGGCCTCCTCTGGGGCTCAGGGCCCTGGC  
 1 CGGCTTCGGCGACCTCATGGGTACATACCCCTCGTCCGGCGCCCCCTCTGGAGGGCTGCCAGGGCCCTGGC  
 1 CGGCTTCGGCGACCTCATGGGTACATACCCCTCGTCCGGCGCCCCCTCTGGAGGGCTGCCAGGGCCCTGGC

73 GCATGGCGTCCGGTTCTGAAAGACGGCGTGAACATGCAACAGGGAACCTTCCCTGGTGCCTCTCTAT  
 73 GCATGGCGTCCGGTTCTGAAAGACGGCGTGAACATGCAACAGGGAACCTTCCCTGGTGCCTCTCTAT  
 73 GCACGGCGTCCGGTTCTGAAAGACGGCGTGAACATGCAACAGGGAACCTTCCCTGGTGCCTCTCTAT

145 CTTCCCTTCGGCTCTGCTCTTGCTGCGGATCGGCCGATCGGCCGATCGGCCGATCGGCCGATCGGCCGAT  
 145 CTTCCCTTCGGCCCTGCTCTTGACTGTGACTGTGCCGCTACCGGCAACTCCACGGGCT  
 145 CTTCCCTTCGGCCCTaCTCTCTGCGGCTGCGGCTACGCCGATCCAAGTGGCAACTCTACGGGGCT

217 TTACCATGTCACCAATGATGCCCTAATCGAGTATGTTACGAGacCCATCCTAcACTCTCC  
 217 TTACCACTTCACCAATGATGCCCTAATCGAGTATGTTACGAGTATGCCCTGCAcCTCC  
 217 TTACCATGTCACCAATGATGCCCTAATCGAGTATGTTACGAGTATGCCCTGCAcCTCC

289 GGGGTGtGTCCTTGGCTTGGGAGGGAAAGCCCTGGCTGGGTTGGGGTGGCCAC  
 289 GGGGTGCGGTCCCTTGGCTGAGGGCAAGGCCCTGGCTGGGTTGGGGTGGCCAC  
 289 GGGGTGtGTCCTTGGCTTGGGAGGGAAAGCCCTGGCTGGGTTGGGGTGGCCAC

289 GGGGTGtGTCCTTGGCTTGGGAGGGAAAGCCCTGGCTGGGTTGGGGTGGCCAC

**FIG.5-2**

361 CAGGGACGGCAACCTCCCCGCAACGCGCTTTCGACGTCACATCGATCTGGCTTGTCGGAGtGCCACCCCTtTG  
361 CAGGGAtGGCAAACTCCCCGCGAGCGAGCTTCGACGTCACATCGATCTGGCTTGTCGGAGGCCACCCCTCTG  
361 CAaggAACGGCAAACCTCCCCaCaACGCGAGCTTCGACGTCACATCGATCTGGCTTGTCGGAGGCCACCCCTCTG  
433 CTGGGCCCTCTATGTGGGGACT-TGTGGGGTCTGTCCTTTCTTGTGGGtRACTGTTCACTtTTCTCCCAAG  
433 tTGGGCCCTCTACGTGGGGACCTGTGGGGTCTGTCCTTTCTTGTGGGtCAACTGTTCACTTCTCCCAAG  
433 CTGGGCCCTCTACGGGGACCTtGGGGTCCatCTTCTTGTGGtCAACTGTTlACCTTCTCTCCCAAG  
505 GCGCCACTGGACACGGAAAGGAtTGAACtGCAACTGCTCTATCTACCCGGCCATAAACGGGAcACCGCAGGGCATG  
505 GCGCCACTGGACGGCAAGGtTGCRAAtTGCCTCTATCTATCCGGCCATAAACGGGtCACGGCATGGCATG<sup>15</sup>  
505 GCGCCACTGGACGGCAAGGtTGCRAAtTCTATCTATCCGGCCATAAACGGGtCACGGCATGGCATG<sup>23</sup>  
577 GGATATGATGATGATGAACtGGTCCCTACAgCaggCCCTACGAGCAGGtTGGTAATGGCTCAGtGCTCAGGATCCCtCAAGCCAT  
577 GGATATGATGATGATGAACtGGTCCCTACGAGCAGGtTGGTAATGGCTCAGGtGCTCAGGtTGGGATCCCAAGCCAT  
577 GGATATGATGATGAACtGGTCCCTACGAGCAGGtTGGTAATGGCTCAGGtGCTCAGGtTGGGATCCCAAGCCAT  
649 CTTGGACATGATGCTGGTGTGCTCACTGGGAGtTCAGGGCTAGCGGGCATAGGGTATTTCCTCCATGGTGGGAACtG  
649 CTTGGACATGATGCTGGTGTGCTCACTGGGAGtTCAGGGCTAGCGGGCATAGGGTATTTCCTCCATGGTGGGAACtG  
721 GGGAAAGGtCCtGGTGTGCTGtGCTGTTGCGGtGCAACtAaccAtaccACCCGGGGGAAatG  
721 GGCAGAAGGtCCTGGTAGtGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
721 GGCAGAAGGtCCTGGTAGtGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG

793 tGCCaggACCacGcagGcgCTcacAGttttTCAGCCAGGGCCAGGAGGAtatCCAGGTGATCAACAC  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 793 CGGCCacACTgtGtCTGGATTGCTCAGGCTCTCGACCCAGGGCCAGGAGAACGtCCAGGTGATCAACAC  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 793 CGCCGAGGcacGCTGGAGTTGCTAGtCTCTCACACCGGGCTAGGAGAACatTCCAGGTGATCAACAC  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
  
 865 CAACGGCAAGTTGGCACATCAATCGCACGGCCttGAACtGAAATGcgAGGCCTCGACActGGCTGGTaaGG  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 865 CAACGGCAAGTTGGCACCTCAATAAGCACGGCCCTGAACtGCAATGATAAGCCTCAACCCGGCTGCTTGGCaGG  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 865 CAACGGCAAGTTGGCACatCAATAAGtACGGCCTtGAACtGCAATGACAAGCCttACCCGGCTtACCCCTaGGGG  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
  
 937 GCTctttCTATTACCAAAATTCAACTCTTAGGCTGCCCCGAGAGGAAtGGCCAGGAtTggGCCAGCTGtaGGCCCCCTtgCCGA  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 937 GCTtttCTATTACCAAAATTCAACTCTTAGGCTTCCtGAGAGGGtAGCCAGCTGCCCAGCCCTTAACCGA  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 937 GCTtttCTATTACCAAAATTCAACTCTTAGGCTGtCCCGAGAGGGtTggGCCAGCTGCCCAGCCCTAACCGA  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
  
 1009 TTtGACCAAGG  
 \* \* \* \* \* \* \* \* \*  
 1009 TTtGACCAAGG  
 \* \* \* \* \* \* \* \* \*  
 1009 TTtGCCCAAGG

FIG.5-3

## SUBSTITUTE SHEET

**FIG. 6**

1 GFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVASAYQVRNSSGI  
 1 GFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVASAYQVRNSTGL  
 1 GFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVASAYQVRNSTGL  
 73 YHVTNDCPNNSIVYETADTILHSPGCCVPCVREGNASkCWVpvapTVATRDGNLPATQRLRKHIDLLVGSATLC  
 73 YHVTNDCPNNSIVYEAADAILHAPGCCVPCVREGNASRCHVANTPTVATRDGKLPATQRLRKHIDLLVGSATLC  
 73 YHVTNDCPNNSIVYEAADAILHAPGCCVPCVREDNVSRCHVAVTPVATRDGKLPtTQLRRHIDLLVGSATLC  
 145 SALYVGDLCGSVFLVGOLFTSPPRHWTQDNCNSIYPGHITGHRMAWDMMNNWSPTtaALVMAOLLRIPOAI  
 145 SALYVGDLCGSVFLVGOLFTSPPRHWTQGNCNSIYPGHITGHRMAWDMMNNWSPTtALVMAOLLRIPOAI  
 145 SALYVGDLCGSVFLVGOLFTSPPRHWTQDNCNSIYPGHITGHRMAWDMMNNWSPTtaALVMAOLLRIPOAI  
 217 LDMDIAGAHWGVLAGIAYFSMVGNWAKVLVYLIFAGVDATTyTtGGNaartqgaltSffsPGAKQdIQLINT  
 217 LDMDIAGAHWGVLAGIAYFSMVGNWAKVLVYLIFAGVDATTyTtGGSAghTvStGfvSLLaPGAKONVOLINT  
 217 LDMDIAGAHWGVLAGMAYFSMVGNWAKVLVYLIFAGVDAAETHtTGSAAarstaGvaSLftPGAFQNIQLINT  
 289 NGSWHINrTALNCNASLdTGWVAGLFYYHKFNSSGCPERMASCRPLAdFD0  
 289 NGSWHINSTALNCNDSLntGWLAGLFYHHKENSSGGPERLASCRPLTDfd0 1. human 27  
 289 NGSWHINSTALNCNDSLttGWLAGLFYHHKENSSGGPERLASCRPLTDfaQ 2. HCV 1 3. human 23

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CLUSTERED PAIR-WISE 'REGION' ALIGNMENT  
in 'identity (no translation)' alphabet of:

- 1. ssThorn#8.r (1-587)
  - 2. sSEC1#2.r (1-587)
  - 3. ssHCT18#7.r (1-587)
  - 4. env1.hcv (1-1657)
- 1  
1  
1

FIG.7-1

GA  
GA  
GA

289 gggtggcggatggctccctgtctcccgtagctcgccctacagaccggccggtaGg

3 ATTGGCAATTGGTAAGGTCAACCTTACGATCGGCTTCCGGACCTCATGGGTACATAACCCTC / 18  
3 ATTGGCAATTGGTAAGGTCAACCTTACGATCGGCTTCCGGACCTCATGGGTACATAACCCTC / 23  
3 ATTGGCAATTGGTAAGGTCAACCTTACGATCGGCTTCCGGACCTCATGGGTACATAACCCTC  
361 tcggCGCAATTGGTAAGGTCAACCTTACGATCGGCTTCCGGACCTCATGGGTACATAACCCTC

75 GTCGGGCCCTTTCGGGCCATGGCTCCGGTCTGGAAAGACGGCGTGAAC  
75 GTCGGGCCCTTTCGGGCCATGGCTCCGGTCTGGAAAGACGGCGTGAAC  
75 GTCGGGCCCTTTCGGGCCATGGCTCCGGTCTGGAAAGACGGCGTGAAC  
433 GTCGGGCCCTTTCGGGCCATGGCTCCGGTCTGGAAAGACGGCGTGAAC

**FIG. 7-2**

147 TATGCAACAGGAACCT'TCCTGGTGTCTTCTCCTCTGCCCTGCTCTCTTGtCTGACCCGTG  
147 TATGCAACAGGAACCT'TCCTGGTGTCTCCTCTGGCTCTTGCTCTTGACTGTG  
147 TATGC CAGGGAAACCTTCCTGGTGTCTCTCTATCTCTGGCTCTTGCTCTTGACTGTG  
505 TATGCAACAGGAACCTTCCTGGTGTCTCTGGCTCTTGCTCTTGACTGTG  
219 CCCGCTTACGCCTACCAAGTGGCAACTCCaCGGGGCTTTACCATGTCACCAACGGATTTGGCCCAACTCGAGT  
219 CCCGCTTACGCCTACCAAGTGGCAACTCCaCGGGGCTTTACCATGTCACCAATGATTTGGCCCAACTCGAGT 19 / 23  
219 CCCGCTTACGCCTACCAAGTGGCAACTCCaCGGGGCTTTACCATGTCACCAATGATTTGGCCCAACTCGAGT  
577 CCCGCTTACGCCTACCAAGTGGCAACTCCaCGGGGCTTTACCATGTCACCAATGATTTGGCCCAACTCGAGT  
291 ATTGTGTACGGAGGGCCGATGCCATCCTGCAAGCTCCGGGTGTTGGCTTCGGTGGGGtAACGCC  
291 ATTGTGTACGGAGGGCCGATGCCATCCTGCAACACTCCGGGTGTTGGCTTCGGTGGGGCAACGCC  
291 ATTGTGTACGAAGGGCCGACGCCATCCTGCAACACTCCGGGTGTTGGCTTCGGTGGGGCAACGCC  
649 ATTGTGTACGAAGGGCCGATGCCATCCTGCAACACTCCGGGTGTTGGCTTCGGTGGGGCAACGCCAGCTGG  
363 TCGAGGTGTGGGTGGGATGCCATGCCACGGGAGCTCCCAACGGGAGCTCCCAACGCCAGCTGG  
363 TCGAGGTGTGGGTGGGATGCCATGCCACGGGAGCTCCCAACGGGAGCTCCCAACGCCAGCTGG  
363 TCGAGGTGTGGGTGGGATGCCATGCCACGGGAGCTCCCAACGGGAGCTCCCAACGCCAGCTGG  
721 TCGAGGTGTGGGTGGGAGGCCACGGGATGCCATGCCACGGGAGCTCCCAACGCCAGCTGG  
721 TCGAGGTGTGGGTGGGAGGCCACGGGAGCTCCCAACGCCAGCTGG

435 CGTCACATCGATCTGCTTGTGGGAGCCACCCCTCTGCTGGCCCTCTACGTCGGGACCTGTGGGGTCC  
435 CGTCACATCGATCTGCTTGTGGGAGGCtACCCCTCTGCTGGCCCTCTACGTCGGGACCTGTGGGGTCT  
435 CGTCACATCGATCTGCTTGTGGGAGCCACCCCTCTGCTGGCCCTCTACGTCGGGACTGTGGGGTCT  
793 CGTCACATCGATCTGCTTGTGGGAGCCACCCCTCTGCTGGCCACTGTGGGGACTGTGGGGACTGTGGGGTCT

507 atCTTtCTTGTGGTCAACTGTTCAACCTTCTTCCAGGCCACTGGACGACGGCAAGGTTGCAATTGGCTCT<sup>20/23</sup>  
507 GTCTTCCCTTGTGGTCAACTGTTAACCTTCTTCCAGGCCACTGGACGACGGCAAGGTTGCAATTGGCTCT  
507 GTCTTCTTGTGGCCAACCTTACCTTCTTCCAGGCCACTGGACGACGGCAAGGTTGCAATTGGCTCT  
865 GTCTTCTTGTGGCCAACCTTACCTTCTTCCAGGCCACTGGACGACGGCAAGGTTGCAATTGGCTCT

579 ATCGAATTc  
579 ATCGAATTc  
579 ATCGAATTc  
937 ATCTATCCC

FIG. 7-3

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	10	20	30	40			
EC10	GAATTGGACGACGCAAGGTTGCAATTGCTCTATCTATCCGGCCATAT						
HCV1	X:::::::::::::::::::						
	550	560	570	580			
	590	600					
	50	60	70	80	A	90	100
	AACAGGTCAACCGCATGGCATGGGATATGATGATGAACCTGGTCCCCTACGACGGCGTTAGT						
	610	620	630	640		650	660
	110	120	130	140	150	160	
	GGTAGCTCAGCTGCTCCGGATCCCACAAGCCATCTGGACATGATCGCTGGTGCTCACTG						
	670	680	690	700	710	720	
	170	180	190	200	210	220	
	GGGAGTCCTGGCGGGCATAGCGTATTCATGGTGGGGAACTGGCGAAGGTCTTGGC						
	730	740	750	760	770	780	
	230	240	250	260	270	280	
	AGTGCTGCTGCTATTGCCGGCGTCGACGCCGAAACCCACGTCACTGGGGGGATGCCGC						
	790	800	810	820	830	840	
	290	300	310	320	330	340	
	CAAAACTACGGCTAGCCTTACTGGTCTCTCAATTAGGTGCCAAGCAGAACATCCAGCT						
	850	860	870	880	890	900	
	350	360	370	380	390	400	
	GATCAACACCAACGGCAGTGGCACATCAACAGGACGGCCTGAACTGCAATGATAGCCT						
	910	920	930	940	950	960	
	410	420					
	CAACACCGGCTGGAATTC						
	X						
	CAACACCGGCTGGTGGCAGGGCTTTCTATCACCACAAGTTCAACTCTTCAGGCTGTCC						
	970	980	990	1000	1010	1020	

FIG.8

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AA#300-438 ( C-terminal region of the putative  
amino ~1/3 of NS1)

- 1) JH23 ? envelope region and
- 2) JH27 ?
- 3) Japanese Isolate (T. Miyamura) ?
- 4) EC10 (Italy) 2 clones  
(one nt L  
result in a quenched  
multiple difference, which did not
- 5) HCV-1 (chimpanzee) S ← NS1 amino acid change)

- 1) D
- 2) D
- 3)
- 4)

A V  
A  
VS

5) TTQGCNCISIYPGHIITGHRMAWDMMMNWSPTTALVMAQLLRIPOA, VM V

- |    |     |       |                   |
|----|-----|-------|-------------------|
| 1) | M   | R     | MIAGA             |
| 2) |     | T Y T | A RSTA VA         |
| 3) | L Y | I M   | N A R T Q A L T F |
| 4) |     | G H R | V Q V T T L T     |
| 5) |     | A     | I A K T A S L T A |

5) HWGVLAGIAYFSMVGNWAKVLVVLFFAGVDAETHVTGGSAGHTVSGFVSL

- |        |                                      |     |     |
|--------|--------------------------------------|-----|-----|
| 1) FS  | R I                                  | I   | T V |
| 2) FT  | D I                                  | I R | A D |
| 3) FR  | S K I V                              | I R | Q F |
| 4) FNL | I                                    | I R | N   |
| 5)     | LAPGAKQNVQLINTNGSWHLNSTALNCNDSLNTGWL |     |     |

SUMMARY: NS 1 AA 330-660

"Isolate"      ZHomology (AA330-438)      ZHomology (AA383-405)

JH23	83	57
JH27	80	39
Japanese	73	48
EC10 (Italy)	84	48

FIG. 10

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AA #117-308 (putative envelope region) FIG.9

- |                       |                    |
|-----------------------|--------------------|
| 1) HCT #18 (USA)      | 3 clones sequenced |
| 2) JH23 (USA)         | ?                  |
| 3) JH 27 (USA)        | ?                  |
| 4) PBL-Th (USA)       | 2 clones sequenced |
| 5) EC1 (Italy)        | 3 clones sequenced |
| 6) HCV-1 (chimpanzee) | multiple           |

C/M ← → S

- |    |     |
|----|-----|
| 1) | (P) |
| 2) |     |
| 3) |     |
| 4) |     |
| 5) |     |

6) RNLGKVIDLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNL

- |    |                                                       |   |   |
|----|-------------------------------------------------------|---|---|
| 1) | H                                                     |   |   |
| 2) |                                                       |   |   |
| 3) | S                                                     | T | T |
| 4) | L                                                     |   |   |
| 5) | (F)                                                   | S |   |
| 6) | PGCSFSIFLLALLSCLTVPASAYQVRNSTGLYHVTNDCPNSSIVYEAADAILH |   |   |

- |     |                                                     |   |     |   |   |
|-----|-----------------------------------------------------|---|-----|---|---|
| 1)  | Y                                                   | V | V   | T |   |
| 2)A | D                                                   | V | V   | K | T |
| 3)s |                                                     |   | PVA | N |   |
| 4)A |                                                     |   | A   | R | T |
| 5)  | H                                                   | V |     | T |   |
| 6)  | TPGCVPVCVREGNASRCWVAMPTVATRDGKLPATQLRRHIDLLVGSATLCS |   |     |   |   |

- |    |                                   |   |
|----|-----------------------------------|---|
| 1) |                                   |   |
| 2) | I                                 | D |
| 3) |                                   | D |
| 4) |                                   |   |
| 5) | I                                 |   |
| 6) | ALYVGDLCGSVFLVGQLFTSPRRHWTTQGCNCI |   |

SUMMARY: "S" AA117-308 (93%)

HCT#18, PBL-Th, EC1(Italy) have 97% homology with HCV-1  
 JH23 and JH 27 have 96% and 95% homology with HCV-1,respectively

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